

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
4 October 2001 (04.10.2001)

PCT

(10) International Publication Number  
**WO 01/72774 A2**

- (51) International Patent Classification<sup>7</sup>: **C07K 14/00**
- (21) International Application Number: PCT/GB01/01297
- (22) International Filing Date: 23 March 2001 (23.03.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:  
0007268.6 24 March 2000 (24.03.2000) GB
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- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:**  
— without international search report and to be republished upon receipt of that report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*



**WO 01/72774 A2**

(54) Title: CELL CYCLE PROGRESSION PROTEINS

(57) Abstract: Polynucleotides encoding a number of *Drosophila* gene products are provided. Polynucleotide probes derived from these nucleotide sequences, polypeptides encoded by the polynucleotides and antibodies that bind to the polypeptides are also provided.

## CELL CYCLE PROGRESSION PROTEINS

The present invention relates to a number of genes implicated in the processes of cell cycle progression, including mitosis and meiosis.

We have now identified a large number of genes in *Drosophila*, mutations in  
5 which disrupt cell cycle progression, for example the processes of mitosis and/or meiosis. We have determined the phenotypes of these mutations and recovered nucleotide sequences associated with the corresponding genes. Many of these nucleotide sequences correspond to protein open reading frames (ORFs) present in the *Drosophila* genome.

Accordingly the present invention provides in one aspect a polynucleotide selected  
10 from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 70 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 70, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 70 or  
15 a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

There is provided, according to another aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 14 or the complement thereof; (b) polynucleotides  
20 comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 14, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 14 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined  
25 in (a), (b) or (c).

We provide, according to yet a further aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide

sequences set out in Examples 15 to 19 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 15 to 19, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in  
5 Examples 15 to 19 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

As a further aspect of the present invention, there is provided a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out  
10 in Examples 20 to 30 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 20 to 30, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 20 to 30 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence  
15 which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

We provide, according to a yet further aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 31 to 53 or the complement thereof; (b) polynucleotides  
20 comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 31 to 53, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 31 to 53 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a),  
25 (b) or (c).

The present invention, in a further aspect, provides a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in 54 to 70 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in 54 to 70, or a fragment thereof; (c)

polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 54 to 70 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

- 5           A polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide according to any of the above aspects of the invention.

          The present invention also provides a polypeptide which comprises any one of the amino acid sequences set out in Examples 1 to 70 or in any of Examples 1 to 14, Examples 15 to 19, Examples 20 to 30, Examples 31 to 53 and Examples 54 to 70, or a  
10   homologue, variant, derivative or fragment thereof.

          Preferably the polypeptide is encoded by a cDNA sequence obtainable from a eukaryotic cDNA library, preferably a metazoan cDNA library (such as insect or mammalian) said DNA sequence comprising a DNA sequence being selectively detectable with a *Drosophila* nucleotide sequence as shown in any one of Examples 1 to 70.

- 15           The term “selectively detectable” means that the cDNA used as a probe is used under conditions where a target cDNA of the invention is found to hybridize to the probe at a level significantly above background. The background hybridization may occur because of other cDNAs present in the cDNA library. In this event background implies a level of signal generated by interaction between the probe and a non-specific cDNA  
20   member of the library which is less than 10 fold, preferably less than 100 fold as intense as the specific interaction observed with the target cDNA. The intensity of interaction may be measured, for example, by radiolabelling the probe, e.g. with <sup>32</sup>P. Suitable conditions may be found by reference to the Examples, as well as in the detailed description below.

          A polynucleotide encoding a polypeptide of the invention is also provided.

- 25           The present invention further provides a vector comprising a polynucleotide of the invention, for example an expression vector comprising a polynucleotide of the invention

operably linked to a regulatory sequence capable of directing expression of said polynucleotide in a host cell.

Also provided is an antibody capable of binding a polypeptide of the invention.

5 In a further aspect the present invention provides a method for detecting the presence or absence of a polynucleotide of the invention in a biological sample which method comprises: (a) bringing the biological sample containing DNA or RNA into contact with a probe comprising a nucleotide of the invention under hybridising conditions; and (b) detecting any duplex formed between the probe and nucleic acid in the sample.

10 In another aspect the invention provides a method for detecting a polypeptide of the invention present in a biological sample which comprises: (a) providing an antibody of the invention; (b) incubating a biological sample with said antibody under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said antibody is formed.

15 Knowledge of the genes involved in cell cycle progression allows the development of therapeutic agents for the treatment of medical conditions associated with aberrant cell cycle progression. Accordingly, the present invention provides a polynucleotide of the invention for use in therapy. The present invention also provides a polypeptide of the invention for use in therapy. The present invention further provides an antibody of the  
20 invention for use in therapy.

In a specific embodiment, the present invention provides a method of treating a tumour or a patient suffering from a proliferative disease, comprising administering to a patient in need of treatment an effective amount of a polynucleotide, polypeptide and/or antibody of the invention.

25 The present invention also provides the use of a polypeptide of the invention in a method of identifying a substance capable of affecting the function of the corresponding

gene. For example, in one embodiment the present invention provides the use of a polypeptide of the invention in an assay for identifying a substance capable of inhibiting cell cycle progression. The substance may inhibit any of the steps or stages in the cell cycle, for example, formation of the nuclear envelope, exit from the quiescent phase of the cell cycle (G0), G1 progression, chromosome decondensation, nuclear envelope breakdown, START, initiation of DNA replication, progression of DNA replication, termination of DNA replication, centrosome duplication, G2 progression, activation of mitotic or meiotic functions, chromosome condensation, centrosome separation, microtubule nucleation, spindle formation and function, interactions with microtubule motor proteins, chromatid separation and segregation, inactivation of mitotic functions, formation of contractile ring, and cytokinesis functions. For example, possible functions of genes of the invention for which it may be desired to identify substances which affect such functions include chromatin binding, formation of replication complexes, replication licensing, phosphorylation or other secondary modification activity, proteolytic degradation, microtubule binding, actin binding, septin binding, microtubule organising centre nucleation activity and binding to components of cell cycle signalling pathways.

In a further aspect the present invention provides a method for identifying a substance capable of binding to a polypeptide of the invention, which method comprises incubating the polypeptide with a candidate substance under suitable conditions and determining whether the substance binds to the polypeptide.

In an additional aspect, the invention provides kits comprising polynucleotides, polypeptides or antibodies of the invention and methods of using such kits in diagnosing the presence of absence of polynucleotides and polypeptides of the invention including deleterious mutant forms.

Also provided is a substance identified by the above methods of the invention. Such substances may be used in a method of therapy, such as in a method of affecting cell cycle progression, for example mitosis and/or meiosis.

The invention also provides a process comprising the steps of: (a) performing one of the above methods; and (b) preparing a quantity of those one or more substances identified as being capable of binding to a polypeptide of the invention.

Also provided is a process comprising the steps of: (a) performing one of the above  
5 methods; and (b) preparing a pharmaceutical composition comprising one or more substances identified as being capable of binding to a polypeptide of the invention.

We further provide a method for identifying a substance capable of modulating the function of a polypeptide of the invention or a polypeptide encoded by a polynucleotide of the invention, the method comprising the steps of: incubating the polypeptide with a  
10 candidate substance and determining whether activity of the polypeptide is thereby modulated.

A substance identified by a method or assay according to any of the above methods or processes is also provided, as is the use of such a substance in a method of inhibiting the function of a polypeptide. Use of such a substance in a method of regulating a cell  
15 division cycle function is also provided.

#### **DETAILED DESCRIPTION OF THE INVENTION**

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA and immunology, which are within the capabilities of a person of ordinary skill in  
20 the art. Such techniques are explained in the literature. See, for example, J. Sambrook, E. F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Second Edition, Books 1-3, Cold Spring Harbor Laboratory Press; Ausubel, F. M. et al. (1995 and periodic supplements; *Current Protocols in Molecular Biology*, ch. 9, 13, and 16, John Wiley & Sons, New York, N.Y.); B. Roe, J. Crabtree, and A. Kahn, 1996, *DNA Isolation and Sequencing: Essential Techniques*, John Wiley & Sons; J. M. Polak and James O'D.  
25 McGee, 1990, *In Situ Hybridization: Principles and Practice*, Oxford University Press; M. J. Gait (Editor), 1984, *Oligonucleotide Synthesis: A Practical Approach*, Irl Press; and, D.

M. J. Lilley and J. E. Dahlberg, 1992, *Methods of Enzymology: DNA Structure Part A: Synthesis and Physical Analysis of DNA* Methods in Enzymology, Academic Press. Each of these general texts is herein incorporated by reference.

Preferably, the polypeptides and polynucleotides of the invention are such that they  
 5 give rise to or are associated with defined phenotypes when mutated.

For example, mutations in the polypeptides and polynucleotides of the invention may be associated with a failure to complete cytokinesis; such polypeptides and polynucleotides are conveniently categorised as "Category 1". Phenotypes associated with Category 1 polypeptides and polynucleotides include any one or more of the following,  
 10 singly or in combination: Mitotic defects in brain: cytokinesis defect (polyploidy); Male semi-sterile, Meiotic defects in testis: cytokinesis defects, segregation defects.(Seg-01/62); Meiotic defects in testis: cytokinesis defects, abnormal spindles.(Ab-02/12); Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, high polyploidy); Meiotic defects in testis: cytokinesis defects. Dark bands in eyes, dominant; Meiotic  
 15 defects in testis: cytokinesis defects; Meiotic defects in testis:segregation defect, cytokinesis defect(Ck-09/32); Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, very high polyploidy); Mitotic defects in brain: cytokinesis defect(very high polyploidy); Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects (Mitotic higher level of condensation, polyploidy, Meiotic:  
 20 Ck05/07); Mitotic defects in brain, Cytokinesis defect (no overcondensation of diploids, high polyploidy); Mitotic defects in brain: cytokinesis defect (very high polyploidy, chromosomes entangled?); Mitotic defects in brain: cytokinesis defect (very high polyploidy; Meiotic defects in testis: cytokinesis defects (Ck-04/06) `; Female sterile (anaphase bridges, lagging chromosomes); Mitotic defects in brain: cytokinesis defect.  
 25 Meiotic defects in testis: cytokinesis defects:(mitotic: high polyploidy, no diploids, higher mitotic index, meiotic: Ck-01/05); Meiotic defects in testis: cytokinesis defects; Meiotic defects in testis: cytokinesis defects(Ck-06/09); Meiotic defects in testis: segregation defects, cytokinesis defect(Ck-07/35); Meiotic defects in testis: cytokinesis defects.

Alternatively, mutations in the polypeptides and polynucleotides of the invention may be associated with a failure to enter M-phase; such polypeptides and polynucleotides are conveniently categorised as "Category 2". Phenotypes associated with Category 2 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Meiotic defects in testis: no division(no meiosis); Mitotic defects in brain: no mitosis; Meiotic defects in testis: segregation defects, meiotic failure(Mf-07/75); Meiotic defects in testis: segregation defects, meiotic failure(Mf-05/31); Meiotic defects in testis: cytokinesis defects, meiotic failure(Mf-02/15).

Mutations in the polypeptides and polynucleotides of the invention may be associated with a metaphase arrest phenotype ("Category 3"). Phenotypes associated with Category 3 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Mitotic defects in brain: prometaphase arrest (overcondensation, polyploidy, scattered chromosomes with bipolar spindle); Male sterile, Female sterile, Mitotic defects in brain: prometaphase arrest (Overcondensation, polyploidy, fewer anaphases, high mitotic index, scattered chromosomes with bipolar spindle); Mitotic defects in brain: (weak overcondensation, metaphase with bipolar spindle); Mitotic defects in brain: prometaphase arrest; Mitotic defects in brain: metaphase arrest; Mitotic defects in brain: metaphase arrest. (overcondensation, polyploidy, aneuploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle); Mitotic defects in brain: metaphase arrest.(overcondensation, polyploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle); Mitotic defects in brain: Metaphase arrest (overcondensation, polyploidy, aneuploidy, no anaphases, high mitotic index, metaphase with bipolar spindle); Mitotic defects in brain: metaphase arrest (overcondensation, metaphase with bipolar spindle; Meiotic defects in testis: segregation defects, multipolar spindles (Mul-02/29); Meiotic defects in testis: cytokinesis defects, abnormal spindles.(Ab-01/03); Mitotic defects in brain: metaphase arrest; Mitotic defects in brain: metaphase arrest (overcondensation, polyploidy, metaphase with bipolar spindle); Mitotic defects in brain: metaphase arrest. Meiotic defects in testis: segregation defects. Abnormal spindles (mitotic: High mitotic index, meiotic: Ab-08/24); Mitotic defects in brain: metaphase arrest(overcondensation, few anaphases, some polyploids); Mitotic defects in brain: prometaphase arrest (overcondensation, fewer anaphases, metaphase with bipolar spindle);

Mitotic defects in brain: metaphase arrest(condensation, no polyploidy, no anaphases, metaphase with bipolar spindle).

Mutations in Category 4 polypeptides and polynucleotides of the invention may be associated with an anaphase defect phenotype; phenotypes associated with Category 4

5 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Mitotic defects in brain: anaphase defects (overcondensation, high polyploidy, some lagging chromosomes); Meiotic defects in testis: segregation defects; Male and female sterile, small wings, meiotic defects in testis: segregation defects, elongation defect; Mitotic defects in brain: anaphase defects(overcondensation, anaphase

10 bridge, metaphase with swollen chromosomes and bipolar spindle); Mitotic defects in brain: Anaphase defects. (overcondensation, aneuploidy, some lagging chromosomes and breaks); Meiotic defects in testis: segregation defects; Meiotic defects in testis: segregation defects, multi-stage defects (Pl-02/17); Meiotic defects in testis: segregation defects, multi-stage defects (Pl-02/18); Meiotic defects in testis: cytokinesis defects,

15 segregation defects (seg-01/01); Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defect. Multi-stage defects Polyploidy, no overcondensation Pl-01/10; Meiotic defects in testis: segregation defects, abnormal spindles. (Ab-03/30); Mitotic defects in brain: anaphase defects (weak, higher condensation, some polyploidy, fewer anaphases, polyploids with monopolar spindles); Mitotic defects in brain: anaphase

20 defects (overcondensation, polyploidy (with overcondensation), few anaphases, metaphase with bipolar spindle); Meiotic defects in testis: cytokinesis defects; Meiotic defects in testis: segregation defects, multipolar spindles(Mul-02/22); Meiotic defects in testis: segregation defects, abnormal spindles (Ab-04/26); Meiotic defects in testis: cytokinesis defects, abnormal spindles (Ab-16/13); Mitotic defects in brain: anaphase defects. Meiotic

25 defects in testis: segregation defects, abnormal spindles (mitotic : Overcondensation, lagging chromosomes/less aligned metaphase with bipolar spindles, Meiotic: Ab-06/20 ); Meiotic defects in testis: segregation defects; Meiotic defects in testis: no division (no meiosis); Meiotic defects in testis: segregation defects, abnormal spindles (Ab-12/48); Meiotic defects in testis: segregation defects, multipolar spindles(mitotic: High polyploids,

30 no diploids, higher mitotic index Meiotic: Mul-02/59); Meiotic defects in testis: segregation defect; Meiotic defects in testis: segregation defects, abnormal spindles

(meiotic: Ab-08/42); Female sterile. Meiotic defects in testis: cytokinesis defects, segregation defects (Mitotic: Less condensed chromosomes, nuclear bridges, Meiotic: Seg-01/02; Mitotic defects in brain: anaphase defects; Meiotic defects in testis: cytokinesis defects, abnormal spindles (Ab-01/04); Meiotic defects in testis: segregation defects (overcondensation, fewer anaphases); Mitotic defects in brain: (some overcondensation, anaphase bridge, metaphase with swollen chromosome and bipolar spindle).

A fifth category ("Category 5") of polypeptides and polynucleotides of the invention are associated with the presence of small imaginal discs (block to proliferation). Phenotypes associated with Category 5 polypeptides and polynucleotides include any one or more of the following, singly or in combination: 2nd chromosome, small imaginal discs.

The polypeptides and polynucleotides of the invention may also be categorised according to their function, or their putative function.

For example, the polypeptides described here preferably comprise, and the polynucleotides described here are ones which preferably encode polypeptides comprising, any one or more of the following: a CBP activator protein; a CCR4-associated regulator of polymerase II transcription; a CTP synthase (CTPS); a Cyclin specific ubiquitin conjugating enzyme; a DNA packaging protein; a DNA repair protein; a DNA-binding protein involved in chromosomal organisation; a DNase IV; a EIF4G2 translation initiation factor; a eukaryotic translation initiation factor 6; a Ecdysone-induced protein 78C; a Egf2 translation factor; a G protein-coupled receptor kinase 7; a GTPase exchange factor; a phosphatidylinositol transfer protein beta isoform; a His-rich protein; a Lk6 kinase; a MAP kinase; a MAP kinase interacting kinase 1; a N-arginine dibasic convertase; a Phosphatidylinositol transfer protein; a RIP protein kinase; a RNA binding motif, single stranded interacting protein; a RNA binding protein; a RYK receptor tyrosine kinase; a Ribosomal protein L1; a selenide, water dikinase 1; a selenium donor protein 1; a selenophosphate synthetase 1; a Sqv-7-like protein; a sugar modification protein; a protein involved in cytokinesis and signalling; a TEK tyrosine kinase; a Translation elongation

factor; a UDP-galactose transporter; a v-erba related protein; a WD40 protein; a brahma protein; a calcium binding protein; a cell adhesion protein; a chaperone; a chromodomain helicase DNA binding protein; a chromodomain-helicase-DNA-binding protein; a coiled coil protein with ubiquitin like domain; a component of the 19S proteasome regulatory particle; a couch potato RNA binding protein; a cytidine 5-prime triphosphate synthetase; a cytoskeletal structural protein; a death domain containing protein; a developmentally expressed in axons of the CNS; a diacylglycerol-activated/phospholipid dependent protein kinase C inhibitor; a diazepam binding inhibitor; a diphosphate kinase; a dodecasattelite DNA binding protein; a doughnut protein tyrosine kinase; an elongation factor 2; a endoplasmic reticulum ATPase; a eukaryotic translation initiation factor 4E binding protein 2; a factor involved in axon guidance; a fatty-acid-Coenzyme A ligase; a flap structure-specific endonuclease 1; a protein involved in the formation of the contractile ring and the initiation of cytokinesis; a glucose-6-phosphate transporter; a glycoprotein glucosyltransferase; a growth factor; a transmembrane receptor protein tyrosine kinase involved in cell growth and maintenance; a guanyl-nucleotide exchange factor involved in signal transduction; a heat shock protein; a helicase; a high density lipoprotein binding protein; a histone acetyl transferase transcriptional activator; a histone acetyltransferase; a histone acetyltransferase GCN5; a protein involved in development of the abdomen (embryos); a protein involved in the development of the imaginal discs (larvae or pupae); a kinesin like protein 67a; a ligand-dependent nuclear receptor; a ligand-dependent nuclear receptor; a lola-like specific RNA polymerase II transcription factor; a matrix associated protein; a membrane glycoprotein; a mitotic heterochromatin fragment clone CH(2)6; a motor protein; a motor protein involved in cytoskeleton organization; a mushroom body RNA binding protein; a myosin like proteins; a nemo-like kinase; a non-ATPase protein; a nuclear receptor NR1E1; a nucleic acid binding protein; a nucleoside diphosphate kinase (NBR-A); a oly(rC)-binding protein 2 (hnRNP-E1); a peroxisome biogenesis factor 1; a phospholipid transporter involved in lipid metabolism; a phosphatase or enhancer of Pi uptake protein; a protease; a proteasome regulatory particle; a protein involved in cytoskeleton organization and/or biogenesis; a protein kinase associated with microtubules; a protein kinase mitogen-activated 7; a protein serine/threonine kinase involved in cell cycle, possibly targeted to cytoskeleton; a protein serine/threonine kinase involved in eye morphogenesis; a protein which associates with cdc25 phosphatase; a

protein which induces apoptosis; a ribonuclease P; a ribonuclease P protein subunit p29; a ser/thr phosphatase; a signal transduction protein; a signal transport protein; a sin3-associated polypeptide; a single stranded DNA/RNA binding protein; a sodium-dependent dicarboxylate transporters; a ssDNA/RNA binding proteins; a striatin, calmodulin-binding protein (STRN); a structural protein of ribosome involved in protein biosynthesis; a subtelomeric heterochromatin repeats; a sugar acetylase; a sugar modification protein; a suppressor of ras; a tRNA processing enzyme Ribonuclease P protein subunit; a thyroid hormone responsive gene; a tie receptor protein tyrosine kinase; a transacylase; a transcription factor; a transcription factor involved in chromatin remodelling; a transcriptional regulation of c-myc expression; a transcriptional regulator; a transcriptional regulators/telomeric silencing; a translation initiation factor; a tumor metastasis inhibitor; a tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; a ubiquitin carrier protein; a ubiquitin-conjugating enzyme; a ugtUDP-glucose-glycoprotein glucosyltransferase; a zinc finger protein; an RNA polymerase II transcription factor; an acetylcholinesterase (YT blood group) precursor; an actin binding protein; an actin dependent regulator of chromatin; an acyl-CoA-binding protein; an alanine:glyoxylate aminotransferase; an alpha esterase; an ankyrin protein; an imitation-SWI protein; and an integrin beta 4 binding protein.

## POLYPEPTIDES

It will be understood that polypeptides of the invention are not limited to polypeptides having the amino acid sequence set out in Examples 1 to 70 or fragments thereof but also include homologous sequences obtained from any source, for example related viral/bacterial proteins, cellular homologues and synthetic peptides, as well as variants or derivatives thereof.

Thus polypeptides of the invention also include those encoding homologues from other species including animals such as mammals (e.g. mice, rats or rabbits), especially primates, more especially humans. More specifically, homologues included within the scope of the invention include human homologues.

Thus, the present invention covers variants, homologues or derivatives of the amino acid sequence set out in Examples 1 to 70, as well as variants, homologues or derivatives of the nucleotide sequence coding for the amino acid sequences of the present invention.

5 In the context of the present invention, a homologous sequence is taken to include an amino acid sequence which is at least 15, 20, 25, 30, 40, 50, 60, 70, 80 or 90% identical, preferably at least 95 or 98% identical at the amino acid level over at least 50 or 100, preferably 200, 300, 400 or 500 amino acids with any one of the polypeptide sequences shown in the Examples. In particular, homology should typically be considered  
10 with respect to those regions of the sequence known to be essential for protein function rather than non-essential neighbouring sequences. This is especially important when considering homologous sequences from distantly related organisms.

Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/functions), in the context of the present  
15 invention it is preferred to express homology in terms of sequence identity.

Homology comparisons can be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These publicly and commercially available computer programs can calculate % homology between two or more sequences.

% homology may be calculated over contiguous sequences, i.e. one sequence is  
20 aligned with the other sequence and each amino acid in one sequence directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues (for example less than 50 contiguous amino acids).

25 Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion will cause the following amino acid residues to be put out of alignment, thus

potentially resulting in a large reduction in % homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting “gaps” in the sequence alignment to try to maximise local homology.

However, these more complex methods assign “gap penalties” to each gap that occurs in the alignment so that, for the same number of identical amino acids, a sequence alignment with as few gaps as possible - reflecting higher relatedness between the two compared sequences - will achieve a higher score than one with many gaps. “Affine gap costs” are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example when using the GCG Wisconsin Bestfit package (see below) the default gap penalty for amino acid sequences is -12 for a gap and -4 for each extension.

Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A; Devereux *et al.*, 1984, Nucleic Acids Research 12:387). Examples of other software than can perform sequence comparisons include, but are not limited to, the BLAST package (see Ausubel *et al.*, 1999 *ibid* – Chapter 18), FASTA (Atschul *et al.*, 1990, J. Mol. Biol., 403-410) and the GENEWORKS suite of comparison tools. Both BLAST and FASTA are available for offline and online searching (see Ausubel *et al.*, 1999 *ibid*, pages 7-58 to 7-60). However it is preferred to use the GCG Bestfit program.

Although the final % homology can be measured in terms of identity, the alignment process itself is typically not based on an all-or-nothing pair comparison. Instead, a scaled similarity score matrix is generally used that assigns scores to each

pairwise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix - the default matrix for the BLAST suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied (see user manual for  
5 further details). It is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.

Once the software has produced an optimal alignment, it is possible to calculate % homology, preferably % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

10 The terms "variant" or "derivative" in relation to the amino acid sequences of the present invention includes any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) amino acids from or to the sequence providing the resultant amino acid sequence retains substantially the same activity as the unmodified sequence, preferably having at least the same activity as the polypeptides presented in the  
15 sequence listings in the Examples.

Polypeptides having the amino acid sequence shown in the Examples, or fragments or homologues thereof may be modified for use in the present invention. Typically, modifications are made that maintain the biological activity of the sequence. Amino acid substitutions may be made, for example from 1, 2 or 3 to 10, 20 or 30 substitutions  
20 provided that the modified sequence retains the biological activity of the unmodified sequence. Alternatively, modifications may be made to deliberately inactivate one or more functional domains of the polypeptides of the invention. Amino acid substitutions may include the use of non-naturally occurring analogues, for example to increase blood plasma half-life of a therapeutically administered polypeptide.

25 Conservative substitutions may be made, for example according to the Table below. Amino acids in the same block in the second column and preferably in the same line in the third column may be substituted for each other:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
AROMATIC		H F W Y

Polypeptides of the invention also include fragments of the full length sequences mentioned above. Preferably said fragments comprise at least one epitope. Methods of identifying epitopes are well known in the art. Fragments will typically comprise at least 6 amino acids, more preferably at least 10, 20, 30, 50 or 100 amino acids.

5 Proteins of the invention are typically made by recombinant means, for example as described below. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. Proteins of the invention may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis,  
 10 GAL4 (DNA binding and/or transcriptional activation domains) and  $\beta$ -galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences. Preferably the fusion protein will not hinder the function of the protein of interest sequence. Proteins of the invention may also be obtained by purification of cell extracts  
 15 from animal cells.

Proteins of the invention may be in a substantially isolated form. It will be understood that the protein may be mixed with carriers or diluents which will not interfere with the intended purpose of the protein and still be regarded as substantially isolated. A protein of the invention may also be in a substantially purified form, in which case it will  
 20 generally comprise the protein in a preparation in which more than 90%, e.g. 95%, 98% or 99% of the protein in the preparation is a protein of the invention.

A polypeptide of the invention may be labeled with a revealing label. The revealing label may be any suitable label which allows the polypeptide to be detected. Suitable labels include radioisotopes, e.g.  $^{125}\text{I}$ , enzymes, antibodies, polynucleotides and linkers such as biotin. Labeled polypeptides of the invention may be used in diagnostic procedures such as immunoassays to determine the amount of a polypeptide of the invention in a sample. Polypeptides or labeled polypeptides of the invention may also be used in serological or cell-mediated immune assays for the detection of immune reactivity to said polypeptides in animals and humans using standard protocols.

A polypeptide or labeled polypeptide of the invention or fragment thereof may also be fixed to a solid phase, for example the surface of an immunoassay well or dipstick. Such labeled and/or immobilised polypeptides may be packaged into kits in a suitable container along with suitable reagents, controls, instructions and the like. Such polypeptides and kits may be used in methods of detection of antibodies to the polypeptides or their allelic or species variants by immunoassay.

Immunoassay methods are well known in the art and will generally comprise: (a) providing a polypeptide comprising an epitope bindable by an antibody against said protein; (b) incubating a biological sample with said polypeptide under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said polypeptide is formed.

Polypeptides of the invention may be used in *in vitro* or *in vivo* cell culture systems to study the role of their corresponding genes and homologues thereof in cell function, including their function in disease. For example, truncated or modified polypeptides may be introduced into a cell to disrupt the normal functions which occur in the cell. The polypeptides of the invention may be introduced into the cell by *in situ* expression of the polypeptide from a recombinant expression vector (see below). The expression vector optionally carries an inducible promoter to control the expression of the polypeptide.

The use of appropriate host cells, such as insect cells or mammalian cells, is expected to provide for such post-translational modifications (e.g. myristolation,

glycosylation, truncation, lapidation and tyrosine, serine or threonine phosphorylation) as may be needed to confer optimal biological activity on recombinant expression products of the invention. Such cell culture systems in which polypeptides of the invention are expressed may be used in assay systems to identify candidate substances which interfere  
5 with or enhance the functions of the polypeptides of the invention in the cell.

## POLYNUCLEOTIDES

Polynucleotides of the invention include polynucleotides that comprise any one or more of the nucleic acid sequences set out in Examples 1 to 70 and fragments thereof. Polynucleotides of the invention also include polynucleotides encoding the polypeptides  
10 of the invention. It will be understood by a skilled person that numerous different polynucleotides can encode the same polypeptide as a result of the degeneracy of the genetic code. In addition, it is to be understood that skilled persons may, using routine techniques, make nucleotide substitutions that do not affect the polypeptide sequence encoded by the polynucleotides of the invention to reflect the codon usage of any  
15 particular host organism in which the polypeptides of the invention are to be expressed.

Polynucleotides of the invention may comprise DNA or RNA. They may be single-stranded or double-stranded. They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to oligonucleotides are known in the art. These include methylphosphonate  
20 and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art. Such modifications may be carried out in order to enhance the *in vivo* activity or life span of polynucleotides of the invention.

25 The terms "variant", "homologue" or "derivative" in relation to the nucleotide sequence of the present invention include any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the

sequence. Preferably said variant, homologues or derivatives code for a polypeptide having biological activity.

As indicated above, with respect to sequence homology, preferably there is at least 50 or 75%, more preferably at least 85%, more preferably at least 90% homology to the sequences shown in the sequence listing herein. More preferably there is at least 95%, more preferably at least 98%, homology. Nucleotide homology comparisons may be conducted as described above. A preferred sequence comparison program is the GCG Wisconsin Bestfit program described above. The default scoring matrix has a match value of 10 for each identical nucleotide and -9 for each mismatch. The default gap creation penalty is -50 and the default gap extension penalty is -3 for each nucleotide.

The present invention also encompasses nucleotide sequences that are capable of hybridising selectively to the sequences presented herein, or any variant, fragment or derivative thereof, or to the complement of any of the above. Nucleotide sequences are preferably at least 15 nucleotides in length, more preferably at least 20, 30, 40 or 50 nucleotides in length.

The term "hybridization" as used herein shall include "the process by which a strand of nucleic acid joins with a complementary strand through base pairing" as well as the process of amplification as carried out in polymerase chain reaction technologies.

Polynucleotides of the invention capable of selectively hybridising to the nucleotide sequences presented herein, or to their complement, will be generally at least 70%, preferably at least 80 or 90% and more preferably at least 95% or 98% homologous to the corresponding nucleotide sequences presented herein over a region of at least 20, preferably at least 25 or 30, for instance at least 40, 60 or 100 or more contiguous nucleotides.

The term "selectively hybridizable" means that the polynucleotide used as a probe is used under conditions where a target polynucleotide of the invention is found to hybridize to the probe at a level significantly above background. The background

hybridization may occur because of other polynucleotides present, for example, in the cDNA or genomic DNA library being screening. In this event, background implies a level of signal generated by interaction between the probe and a non-specific DNA member of the library which is less than 10 fold, preferably less than 100 fold as intense as the  
5 specific interaction observed with the target DNA. The intensity of interaction may be measured, for example, by radiolabelling the probe, e.g. with  $^{32}\text{P}$ .

Hybridization conditions are based on the melting temperature ( $T_m$ ) of the nucleic acid binding complex, as taught in Berger and Kimmel (1987, Guide to Molecular Cloning Techniques, Methods in Enzymology, Vol 152, Academic Press, San Diego CA), and  
10 confer a defined "stringency" as explained below.

Maximum stringency typically occurs at about  $T_m - 5^\circ\text{C}$  ( $5^\circ\text{C}$  below the  $T_m$  of the probe); high stringency at about  $5^\circ\text{C}$  to  $10^\circ\text{C}$  below  $T_m$ ; intermediate stringency at about  $10^\circ\text{C}$  to  $20^\circ\text{C}$  below  $T_m$ ; and low stringency at about  $20^\circ\text{C}$  to  $25^\circ\text{C}$  below  $T_m$ . As will be understood by those of skill in the art, a maximum stringency hybridization can be used to  
15 identify or detect identical polynucleotide sequences while an intermediate (or low) stringency hybridization can be used to identify or detect similar or related polynucleotide sequences.

In a preferred aspect, the present invention covers nucleotide sequences that can hybridise to the nucleotide sequence of the present invention under stringent conditions  
20 (e.g.  $65^\circ\text{C}$  and  $0.1\times\text{SSC}$  { $1\times\text{SSC} = 0.15\text{ M NaCl}$ ,  $0.015\text{ M Na}_3\text{ Citrate pH } 7.0$ }).

Where the polynucleotide of the invention is double-stranded, both strands of the duplex, either individually or in combination, are encompassed by the present invention. Where the polynucleotide is single-stranded, it is to be understood that the complementary sequence of that polynucleotide is also included within the scope of the present invention.

25 Polynucleotides which are not 100% homologous to the sequences of the present invention but fall within the scope of the invention can be obtained in a number of ways. Other variants of the sequences described herein may be obtained for example by probing

DNA libraries made from a range of individuals, for example individuals from different populations. In addition, other viral/bacterial, or cellular homologues particularly cellular homologues found in mammalian cells (e.g. rat, mouse, bovine and primate cells), may be obtained and such homologues and fragments thereof in general will be capable of

5 selectively hybridising to the sequences shown in the Examples. Such sequences may be obtained by probing cDNA libraries made from or genomic DNA libraries from other animal species, and probing such libraries with probes comprising all or part of any one of the sequences shown in the Examples under conditions of medium to high stringency. The nucleotide sequences of the human homologues described in the Examples, may

10 preferably be used to identify other primate/mammalian homologues since nucleotide homology between human sequences and mammalian sequences is likely to be higher than is the case for the *Drosophila* sequences identified herein.

Similar considerations apply to obtaining species homologues and allelic variants of the polypeptide or nucleotide sequences of the invention.

15 Variants and strain/species homologues may also be obtained using degenerate PCR which will use primers designed to target sequences within the variants and homologues encoding conserved amino acid sequences within the sequences of the present invention. Conserved sequences can be predicted, for example, by aligning the amino acid sequences from several variants/homologues. Sequence alignments can be performed

20 using computer software known in the art. For example the GCG Wisconsin PileUp program is widely used.

The primers used in degenerate PCR will contain one or more degenerate positions and will be used at stringency conditions lower than those used for cloning sequences with single sequence primers against known sequences. It will be appreciated by the skilled

25 person that overall nucleotide homology between sequences from distantly related organisms is likely to be very low and thus in these situations degenerate PCR may be the method of choice rather than screening libraries with labeled fragments the sequences disclosed in the Examples.

In addition, homologous sequences may be identified by searching nucleotide and/or protein databases using search algorithms such as the BLAST suite of programs. This approach is described in the Examples.

Alternatively, such polynucleotides may be obtained by site directed mutagenesis of characterised sequences, such as the sequences disclosed in the Examples. This may be useful where for example silent codon changes are required to sequences to optimise codon preferences for a particular host cell in which the polynucleotide sequences are being expressed. Other sequence changes may be desired in order to introduce restriction enzyme recognition sites, or to alter the property or function of the polypeptides encoded by the polynucleotides. For example, further changes may be desirable to represent particular coding changes found in the sequences disclosed in the Examples which give rise to mutant genes which have lost their regulatory function. Probes based on such changes can be used as diagnostic probes to detect such mutants.

Polynucleotides of the invention may be used to produce a primer, e.g. a PCR primer, a primer for an alternative amplification reaction, a probe e.g. labeled with a revealing label by conventional means using radioactive or non-radioactive labels, or the polynucleotides may be cloned into vectors. Such primers, probes and other fragments will be at least 8, 9, 10, or 15, preferably at least 20, for example at least 25, 30 or 40 nucleotides in length, and are also encompassed by the term polynucleotides of the invention as used herein.

Polynucleotides such as a DNA polynucleotides and probes according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques.

In general, primers will be produced by synthetic means, involving a step wise manufacture of the desired nucleic acid sequence one nucleotide at a time. Techniques for accomplishing this using automated techniques are readily available in the art.

Longer polynucleotides will generally be produced using recombinant means, for example using a PCR (polymerase chain reaction) cloning techniques. This will involve making a pair of primers (e.g. of about 15 to 30 nucleotides) flanking a region of the lipid targeting sequence which it is desired to clone, bringing the primers into contact with  
5 mRNA or cDNA obtained from an animal or human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified fragment (e.g. by purifying the reaction mixture on an agarose gel) and recovering the amplified DNA. The primers may be designed to contain suitable restriction enzyme recognition sites so that the amplified DNA can be cloned into a  
10 suitable cloning vector

Polynucleotides or primers of the invention may carry a revealing label. Suitable labels include radioisotopes such as  $^{32}\text{P}$  or  $^{35}\text{S}$ , enzyme labels, or other protein labels such as biotin. Such labels may be added to polynucleotides or primers of the invention and may be detected using by techniques known *per se*.

15 Polynucleotides or primers of the invention or fragments thereof labeled or unlabeled may be used by a person skilled in the art in nucleic acid-based tests for detecting or sequencing polynucleotides of the invention in the human or animal body.

Such tests for detecting generally comprise bringing a biological sample containing DNA or RNA into contact with a probe comprising a polynucleotide or primer of the  
20 invention under hybridising conditions and detecting any duplex formed between the probe and nucleic acid in the sample. Such detection may be achieved using techniques such as PCR or by immobilising the probe on a solid support, removing nucleic acid in the sample which is not hybridised to the probe, and then detecting nucleic acid which has hybridised to the probe. Alternatively, the sample nucleic acid may be immobilised on a  
25 solid support, and the amount of probe bound to such a support can be detected. Suitable assay methods of this and other formats can be found in for example WO89/03891 and WO90/13667.

Tests for sequencing nucleotides of the invention include bringing a biological sample containing target DNA or RNA into contact with a probe comprising a polynucleotide or primer of the invention under hybridising conditions and determining the sequence by, for example the Sanger dideoxy chain termination method (see  
5 Sambrook *et al.*).

Such a method generally comprises elongating, in the presence of suitable reagents, the primer by synthesis of a strand complementary to the target DNA or RNA and selectively terminating the elongation reaction at one or more of an A, C, G or T/U residue; allowing strand elongation and termination reaction to occur; separating out  
10 according to size the elongated products to determine the sequence of the nucleotides at which selective termination has occurred. Suitable reagents include a DNA polymerase enzyme, the deoxynucleotides dATP, dCTP, dGTP and dTTP, a buffer and ATP. Dideoxynucleotides are used for selective termination.

Tests for detecting or sequencing nucleotides of the invention in a biological  
15 sample may be used to determine particular sequences within cells in individuals who have, or are suspected to have, an altered gene sequence, for example within cancer cells including leukaemia cells and solid tumours such as breast, ovary, lung, colon, pancreas, testes, liver, brain, muscle and bone tumours. Cells from patients suffering from a proliferative disease may also be tested in the same way.

20 In addition, the identification of the genes described in the Examples will allow the role of these genes in hereditary diseases to be investigated. In general, this will involve establishing the status of the gene (e.g. using PCR sequence analysis), in cells derived from animals or humans with, for example, neurological disorders or neoplasms.

The probes of the invention may conveniently be packaged in the form of a test kit  
25 in a suitable container. In such kits the probe may be bound to a solid support where the assay format for which the kit is designed requires such binding. The kit may also contain suitable reagents for treating the sample to be probed, hybridising the probe to nucleic acid in the sample, control reagents, instructions, and the like.

## NUCLEIC ACID VECTORS

Polynucleotides of the invention can be incorporated into a recombinant replicable vector. The vector may be used to replicate the nucleic acid in a compatible host cell. Thus in a further embodiment, the invention provides a method of making polynucleotides of the invention by introducing a polynucleotide of the invention into a replicable vector, introducing the vector into a compatible host cell, and growing the host cell under conditions which bring about replication of the vector. The vector may be recovered from the host cell. Suitable host cells include bacteria such as *E. coli*, yeast, mammalian cell lines and other eukaryotic cell lines, for example insect Sf9 cells.

Preferably, a polynucleotide of the invention in a vector is operably linked to a control sequence that is capable of providing for the expression of the coding sequence by the host cell, i.e. the vector is an expression vector. The term "operably linked" means that the components described are in a relationship permitting them to function in their intended manner. A regulatory sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under condition compatible with the control sequences.

The control sequences may be modified, for example by the addition of further transcriptional regulatory elements to make the level of transcription directed by the control sequences more responsive to transcriptional modulators.

Vectors of the invention may be transformed or transfected into a suitable host cell as described below to provide for expression of a protein of the invention. This process may comprise culturing a host cell transformed with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the protein, and optionally recovering the expressed protein. Vectors will be chosen that are compatible with the host cell used.

The vectors may be for example, plasmid or virus vectors provided with an origin of replication, optionally a promoter for the expression of the said polynucleotide and

optionally a regulator of the promoter. The vectors may contain one or more selectable marker genes, for example an ampicillin resistance gene in the case of a bacterial plasmid or a neomycin resistance gene for a mammalian vector. Vectors may be used, for example, to transfect or transform a host cell.

5           Control sequences operably linked to sequences encoding the polypeptide of the invention include promoters/enhancers and other expression regulation signals. These control sequences may be selected to be compatible with the host cell for which the expression vector is designed to be used in. The term promoter is well-known in the art and encompasses nucleic acid regions ranging in size and complexity from minimal  
10 promoters to promoters including upstream elements and enhancers.

The promoter is typically selected from promoters which are functional in mammalian cells, although prokaryotic promoters and promoters functional in other eukaryotic cells, such as insect cells, may be used. The promoter is typically derived from promoter sequences of viral or eukaryotic genes. For example, it may be a promoter  
15 derived from the genome of a cell in which expression is to occur. With respect to eukaryotic promoters, they may be promoters that function in a ubiquitous manner (such as promoters of  $\alpha$ -actin,  $\beta$ -actin, tubulin) or, alternatively, a tissue-specific manner (such as promoters of the genes for pyruvate kinase). They may also be promoters that respond to specific stimuli, for example promoters that bind steroid hormone receptors. Viral  
20 promoters may also be used, for example the Moloney murine leukaemia virus long terminal repeat (MMLV LTR) promoter, the rous sarcoma virus (RSV) LTR promoter or the human cytomegalovirus (CMV) IE promoter.

It may also be advantageous for the promoters to be inducible so that the levels of expression of the heterologous gene can be regulated during the life-time of the cell.  
25 Inducible means that the levels of expression obtained using the promoter can be regulated.

In addition, any of these promoters may be modified by the addition of further regulatory sequences, for example enhancer sequences. Chimeric promoters may also be

used comprising sequence elements from two or more different promoters described above.

Polynucleotides according to the invention may also be inserted into the vectors described above in an antisense orientation to provide for the production of antisense  
5 RNA. Antisense RNA or other antisense polynucleotides may also be produced by synthetic means. Such antisense polynucleotides may be used in a method of controlling the levels of RNAs transcribed from genes comprising any one of the polynucleotides of the invention.

#### HOST CELLS

10 Vectors and polynucleotides of the invention may be introduced into host cells for the purpose of replicating the vectors/polynucleotides and/or expressing the polypeptides of the invention encoded by the polynucleotides of the invention. Although the polypeptides of the invention may be produced using prokaryotic cells as host cells, it is preferred to use eukaryotic cells, for example yeast, insect or mammalian cells, in  
15 particular mammalian cells.

Vectors/polynucleotides of the invention may be introduced into suitable host cells using a variety of techniques known in the art, such as transfection, transformation and electroporation. Where vectors/polynucleotides of the invention are to be administered to animals, several techniques are known in the art, for example infection with recombinant  
20 viral vectors such as retroviruses, herpes simplex viruses and adenoviruses, direct injection of nucleic acids and biolistic transformation.

#### PROTEIN EXPRESSION AND PURIFICATION

Host cells comprising polynucleotides of the invention may be used to express polypeptides of the invention. Host cells may be cultured under suitable conditions which  
25 allow expression of the proteins of the invention. Expression of the polypeptides of the invention may be constitutive such that they are continually produced, or inducible, requiring a stimulus to initiate expression. In the case of inducible expression, protein

production can be initiated when required by, for example, addition of an inducer substance to the culture medium, for example dexamethasone or IPTG.

Polypeptides of the invention can be extracted from host cells by a variety of techniques known in the art, including enzymatic, chemical and/or osmotic lysis and  
5 physical disruption.

Polypeptides of the invention may also be produced recombinantly in an *in vitro* cell-free system, such as the TnT<sup>TM</sup> (Promega) rabbit reticulocyte system.

#### ANTIBODIES

The invention also provides monoclonal or polyclonal antibodies to polypeptides of  
10 the invention or fragments thereof. Thus, the present invention further provides a process for the production of monoclonal or polyclonal antibodies to polypeptides of the invention.

If polyclonal antibodies are desired, a selected mammal (e.g., mouse, rabbit, goat, horse, etc.) is immunised with an immunogenic polypeptide bearing an epitope(s) from a polypeptide of the invention. Serum from the immunised animal is collected and treated  
15 according to known procedures. If serum containing polyclonal antibodies to an epitope from a polypeptide of the invention contains antibodies to other antigens, the polyclonal antibodies can be purified by immunoaffinity chromatography. Techniques for producing and processing polyclonal antisera are known in the art. In order that such antibodies may be made, the invention also provides polypeptides of the invention or fragments thereof  
20 haptenised to another polypeptide for use as immunogens in animals or humans.

Monoclonal antibodies directed against epitopes in the polypeptides of the invention can also be readily produced by one skilled in the art. The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as  
25 direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. Panels of monoclonal antibodies produced against epitopes in the

polypeptides of the invention can be screened for various properties; i.e., for isotype and epitope affinity.

An alternative technique involves screening phage display libraries where, for example the phage express scFv fragments on the surface of their coat with a large variety  
5 of complementarity determining regions (CDRs). This technique is well known in the art.

Antibodies, both monoclonal and polyclonal, which are directed against epitopes from polypeptides of the invention are particularly useful in diagnosis, and those which are neutralising are useful in passive immunotherapy. Monoclonal antibodies, in particular, may be used to raise anti-idiotypic antibodies. Anti-idiotypic antibodies are  
10 immunoglobulins which carry an "internal image" of the antigen of the agent against which protection is desired.

Techniques for raising anti-idiotypic antibodies are known in the art. These anti-idiotypic antibodies may also be useful in therapy.

For the purposes of this invention, the term "antibody", unless specified to the  
15 contrary, includes fragments of whole antibodies which retain their binding activity for a target antigen. Such fragments include Fv, F(ab') and F(ab')<sub>2</sub> fragments, as well as single chain antibodies (scFv). Furthermore, the antibodies and fragments thereof may be humanised antibodies, for example as described in EP-A-239400.

Antibodies may be used in method of detecting polypeptides of the invention  
20 present in biological samples by a method which comprises: (a) providing an antibody of the invention; (b) incubating a biological sample with said antibody under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said antibody is formed.

Suitable samples include extracts tissues such as brain, breast, ovary, lung, colon,  
25 pancreas, testes, liver, muscle and bone tissues or from neoplastic growths derived from such tissues.

Antibodies of the invention may be bound to a solid support and/or packaged into kits in a suitable container along with suitable reagents, controls, instructions and the like.

## ASSAYS

The present invention provides assays that are suitable for identifying substances  
5 which bind to polypeptides of the invention and which affect, for example, formation of the nuclear envelope, exit from the quiescent phase of the cell cycle (G0), G1 progression, chromosome decondensation, nuclear envelope breakdown, START, initiation of DNA replication, progression of DNA replication, termination of DNA replication, centrosome duplication, G2 progression, activation of mitotic or meiotic functions, chromosome  
10 condensation, centrosome separation, microtubule nucleation, spindle formation and function, interactions with microtubule motor proteins, chromatid separation and segregation, inactivation of mitotic functions, formation of contractile ring, cytokinesis functions, chromatin binding, formation of replication complexes, replication licensing, phosphorylation or other secondary modification activity, proteolytic degradation,  
15 microtubule binding, actin binding, septin binding, microtubule organising centre nucleation activity and binding to components of cell cycle signalling pathways.

In addition, assays suitable for identifying substances that interfere with binding of polypeptides of the invention, where appropriate, to components of cell division cycle machinery. This includes not only components such as microtubules but also signalling  
20 components and regulatory components as indicated above. Such assays are typically *in vitro*. Assays are also provided that test the effects of candidate substances identified in preliminary *in vitro* assays on intact cells in whole cell assays. The assays described below, or any suitable assay as known in the art, may be used to identify these substances.

According to one aspect of the invention, therefore, we provide one or more  
25 substances identified by any of the assays described below, viz, mitosis assays, meiotic assays, polypeptide binding assays, microtubule binding/polymerisation assays, microtubule purification and binding assays, microtubule organising centre (MTOC) nucleation activity assays, motor protein assay, assay for spindle assembly and function,

assays for dna replication, chromosome condensation assays, kinase assays, kinase inhibitor assays, and whole cell assays, each as described in further detail below.

#### CANDIDATE SUBSTANCES

A substance that inhibits cell cycle progression as a result of an interaction with a polypeptide of the invention may do so in several ways. For example, if the substance inhibits cell division, mitosis and/or meiosis, it may directly disrupt the binding of a polypeptide of the invention to a component of the spindle apparatus by, for example, binding to the polypeptide and masking or altering the site of interaction with the other component. A substance which inhibits DNA replication may do so by inhibiting the phosphorylation or de-phosphorylation of proteins involved in replication. For example, it is known that the kinase inhibitor 6-DMAP (6-dimethylaminopurine) prevents the initiation of replication (Blow, JJ, 1993, *J Cell Biol*122,993-1002). Candidate substances of this type may conveniently be preliminarily screened by *in vitro* binding assays as, for example, described below and then tested, for example in a whole cell assay as described below. Examples of candidate substances include antibodies which recognise a polypeptide of the invention.

A substance which can bind directly to a polypeptide of the invention may also inhibit its function in cell cycle progression by altering its subcellular localisation and hence its ability to interact with its normal substrate. The substance may alter the subcellular localisation of the polypeptide by directly binding to it, or by indirectly disrupting the interaction of the polypeptide with another component. For example, it is known that interaction between the p68 and p180 subunits of DNA polymerase alpha-primase enzyme is necessary in order for p180 to translocate into the nucleus (Mizuno et al (1998) *Mol Cell Biol*18,3552-62), and accordingly, a substance which disrupts the interaction between p68 and p180 will affect nuclear translocation and hence activity of the primase. A substance which affects mitosis may do so by preventing the polypeptide and components of the mitotic apparatus from coming into contact within the cell. These substances may be tested using, for example the whole cells assays described below. Non-functional homologues of a polypeptide of the invention may also be tested

for inhibition of cell cycle progression since they may compete with the wild type protein for binding to components of the cell division cycle machinery whilst being incapable of the normal functions of the protein or block the function of the protein bound to the cell division cycle machinery. Such non-functional homologues may include naturally occurring mutants and modified sequences or fragments thereof.

Alternatively, instead of preventing the association of the components directly, the substance may suppress the biologically available amount of a polypeptide of the invention. This may be by inhibiting expression of the component, for example at the level of transcription, transcript stability, translation or post-translational stability. An example of such a substance would be antisense RNA or double-stranded interfering RNA sequences which suppresses the amount of mRNA biosynthesis.

Suitable candidate substances include peptides, especially of from about 5 to 30 or 10 to 25 amino acids in size, based on the sequence of the polypeptides described in the Examples, or variants of such peptides in which one or more residues have been substituted. Peptides from panels of peptides comprising random sequences or sequences which have been varied consistently to provide a maximally diverse panel of peptides may be used.

Suitable candidate substances also include antibody products (for example, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies and CDR-grafted antibodies) which are specific for a polypeptide of the invention. Furthermore, combinatorial libraries, peptide and peptide mimetics, defined chemical entities, oligonucleotides, and natural product libraries may be screened for activity as inhibitors of binding of a polypeptide of the invention to the cell division cycle machinery, for example mitotic/meiotic apparatus (such as microtubules). The candidate substances may be used in an initial screen in batches of, for example 10 substances per reaction, and the substances of those batches which show inhibition tested individually. Candidate substances which show activity in *in vitro* screens such as those described below can then be tested in whole cell systems, such as mammalian cells which will be exposed to the inhibitor and tested for inhibition of any of the stages of the cell cycle.

*Polypeptide Binding Assays*

One type of assay for identifying substances that bind to a polypeptide of the invention involves contacting a polypeptide of the invention, which is immobilised on a solid support, with a non-immobilised candidate substance determining whether and/or to what extent the polypeptide of the invention and candidate substance bind to each other. Alternatively, the candidate substance may be immobilised and the polypeptide of the invention non-immobilised.

In a preferred assay method, the polypeptide of the invention is immobilised on beads such as agarose beads. Typically this is achieved by expressing the component as a GST-fusion protein in bacteria, yeast or higher eukaryotic cell lines and purifying the GST-fusion protein from crude cell extracts using glutathione-agarose beads (Smith and Johnson, 1988). As a control, binding of the candidate substance, which is not a GST-fusion protein, to the immobilised polypeptide of the invention is determined in the absence of the polypeptide of the invention. The binding of the candidate substance to the immobilised polypeptide of the invention is then determined. This type of assay is known in the art as a GST pulldown assay. Again, the candidate substance may be immobilised and the polypeptide of the invention non-immobilised.

It is also possible to perform this type of assay using different affinity purification systems for immobilising one of the components, for example Ni-NTA agarose and histidine-tagged components.

Binding of the polypeptide of the invention to the candidate substance may be determined by a variety of methods well-known in the art. For example, the non-immobilised component may be labeled (with for example, a radioactive label, an epitope tag or an enzyme-antibody conjugate). Alternatively, binding may be determined by immunological detection techniques. For example, the reaction mixture can be Western blotted and the blot probed with an antibody that detects the non-immobilised component. ELISA techniques may also be used.

Candidate substances are typically added to a final concentration of from 1 to 1000 nmol/ml, more preferably from 1 to 100 nmol/ml. In the case of antibodies, the final concentration used is typically from 100 to 500 µg/ml, more preferably from 200 to 300 µg/ml.

## 5            ***Microtubule Binding/Polymerisation Assays***

In the case of polypeptides of the invention that bind to microtubules, another type of *in vitro* assay involves determining whether a candidate substance modulates binding of a polypeptide of the invention to microtubules. Such an assay typically comprises contacting a polypeptide of the invention with microtubules in the presence or absence of the candidate substance and determining if the candidate substance has an affect on the binding of the polypeptide of the invention to the microtubules. This assay can also be used in the absence of candidate substances to confirm that a polypeptide of the invention does indeed bind to microtubules. Microtubules may be prepared and assays conducted as follows:

## 15           ***Microtubule Purification and Binding Assays***

Microtubules are purified from 0-3h-old *Drosophila* embryos essentially as described previously (Saunders, *et al.*, 1997). About 3 ml of embryos are homogenized with a Dounce homogenizer in 2 volumes of ice-cold lysis buffer (0.1 M Pipes/NaOH, pH6.6, 5 mM EGTA, 1 mM MgSO<sub>4</sub>, 0.9 M glycerol, 1 mM DTT, 1 mM PMSF, 1 µg/ml aprotinin, 1 µg/ml leupeptin and 1 µg/ml pepstatin). The microtubules are depolymerized by incubation on ice for 15 min, and the extract is then centrifuged at 16,000 g for 30 min at 4°C. The supernatant is recentrifuged at 135,000 g for 90 min at 4°C. Microtubules in this later supernatant are polymerized by addition of GTP to 1 mM and taxol to 20 µM and incubation at room temperature for 30 min. A 3 ml aliquot of the extract is layered on top of 3 ml 15% sucrose cushion prepared in lysis buffer. After centrifuging at 54,000g for 30 min at 20°C using a swing out rotor, the microtubule pellet is resuspended in lysis buffer.

Microtubule overlay assays are performed as previously described (Saunders *et al.*, 1997). 500 ng per lane of recombinant Asp, recombinant polypeptide, and bovine serum albumin (BSA, Sigma) are fractionated by 10% SDS-PAGE and blotted onto PVDF

membranes (Millipore). The membranes are preincubated in TBST (50mM Tris pH 7.5, 150 mM NaCl, 0.05% Tween 20) containing 5% low fat powdered milk (LFPM) for 1 h and then washed 3 times for 15 min in lysis buffer. The filters are then incubated for 30 minutes in lysis buffer containing either 1 mM GDP, 1 mM GTP, or 1 mM GTP- $\gamma$ -S.

- 5 MAP-free bovine brain tubulin (Molecular Probes) is polymerised at a concentration of 2  $\mu$ g/ml in lysis buffer by addition of GTP to a final concentration of 1 mM and incubated at 37°C for 30 min. The nucleotide solutions are removed and the buffer containing polymerised microtubules added to the membranes for incubation for 1h at 37°C with addition of taxol at a final concentration of 10  $\mu$ M for the final 30 min. The blots are then
- 10 washed 3 times with TBST and the bound tubulin detected using standard Western blot procedures using anti- $\beta$ -tubulin antibodies (Boehringer Mannheim) at 2.5  $\mu$ g/ml and the Super Signal detection system (Pierce).

It may be desirable in one embodiment of this type of assay to deplete the polypeptide of the invention from cell extracts used to produce polymerise microtubules.

- 15 This may, for example, be achieved by the use of suitable antibodies.

- A simple extension to this type of assay would be to test the effects of purified polypeptide of the invention upon the ability of tubulin to polymerise *in vitro* (for example, as used by Andersen and Karsenti, 1997) in the presence or absence of a candidate substance (typically added at the concentrations described above). *Xenopus* cell-
- 20 free extracts may conveniently be used, for example as a source of tubulin.

#### ***Microtubule Organising Centre (MTOC) Nucleation Activity Assays***

- Candidate substances, for example those identified using the binding assays described above, may be screening using a microtubule organising centre nucleation activity assay to determine if they are capable of disrupting MTOCs as measured by, for
- 25 example, aster formation. This assay in its simplest form comprises adding the candidate substance to a cellular extract which in the absence of the candidate substance has microtubule organising centre nucleation activity resulting in formation of asters.

In a preferred embodiment, the assay system comprises (i) a polypeptide of the invention and (ii) components required for microtubule organising centre nucleation activity except for functional polypeptide of the invention, which is typically removed by immunodepletion (or by the use of extracts from mutant cells). The components  
5 themselves are typically in two parts such that microtubule nucleation does not occur until the two parts are mixed. The polypeptide of the invention may be present in one of the two parts initially or added subsequently prior to mixing of the two parts.

Subsequently, the polypeptide of the invention and candidate substance are added to the component mix and microtubule nucleation from centrosomes measured, for  
10 example by immunostaining for the polypeptide of the invention and visualising aster formation by immuno-fluorescence microscopy. The polypeptide of the invention may be preincubated with the candidate substance before addition to the component mix. Alternatively, both the polypeptide of the invention and the candidate substance may be added directly to the component mix, simultaneously or sequentially in either order.

15 The components required for microtubule organising centre formation typically include salt-stripped centrosomes prepared as described in Moritz *et al.*, 1998. Stripping centrosome preparations with 2 M KI removes the centrosome proteins CP60, CP190, CNN and  $\gamma$ -tubulin. Of these, neither CP60 nor CP190 appear to be required for microtubule nucleation. The other minimal components are typically provided as a  
20 depleted cellular extract, or conveniently, as a cellular extract from cells with a non-functional variant of a polypeptide of the invention. Typically, labeled tubulin (usually  $\beta$ -tubulin) is also added to assist in visualising aster formation.

Alternatively, partially purified centrosomes that have not been salt-stripped may be used as part of the components. In this case, only tubulin, preferably labeled tubulin is  
25 required to complete the component mix.

Candidate substances are typically added to a final concentration of from 1 to 1000 nmol/ml, more preferably from 1 to 100 nmol/ml. In the case of antibodies, the final

concentration used is typically from 100 to 500 µg/ml, more preferably from 200 to 300 µg/ml.

The degree of inhibition of aster formation by the candidate substance may be determined by measuring the number of normal asters per unit area for control untreated cell preparation and measuring the number of normal asters per unit area for cells treated with the candidate substance and comparing the result. Typically, a candidate substance is considered to be capable of disrupting MTOC integrity if the treated cell preparations have less than 50%, preferably less than 40, 30, 20 or 10% of the number of asters found in untreated cells preparations. It may also be desirable to stain cells for  $\gamma$ -tubulin to determine the maximum number of possible MTOCs present to allow normalisation between samples.

#### ***Motor Protein Assay***

Polypeptides of the invention may interact with motor proteins such as the Eg5-like motor protein *in vitro*. The effects of candidate substances on such a process may be determined using assays wherein the motor protein is immobilised on coverslips. Rhodamine labeled microtubules are then added and their translocation can be followed by fluorescent microscopy. The effect of candidate substances may thus be determined by comparing the extent and/or rate of translocation in the presence and absence of the candidate substance. Generally, candidate substances known to bind to a polypeptide of the invention, would be tested in this assay. Alternatively, a high throughput assay may be used to identify modulators of motor proteins and the resulting identified substances tested for effects on a polypeptide of the invention as described above.

Typically this assay uses microtubules stabilised by taxol (e.g. Howard and Hyman 1993; Chandra and Endow, 1993 – both chapters in “Motility Assays for Motor Proteins” Ed Jon Scholey, pub Academic Press). If however, a polypeptide of the invention were to promote stable polymerisation of microtubules (see above) then these microtubules could be used directly in motility assays.

Simple protein-protein binding assays as described above, using a motor protein and a polypeptide of the invention may also be used to confirm that the polypeptide of the invention binds to the motor protein, typically prior to testing the effect of candidate substances on that interaction.

5           ***Assay for Spindle Assembly and Function***

A further assay to investigate the function of polypeptide of the invention and the effect of candidate substances on those functions is an assay which measures spindle assembly and function. Typically, such assays are performed using *Xenopus* cell free systems, where two types of spindle assembly are possible. In the “half spindle” assembly  
10 pathway, a cytoplasmic extract of CSF arrested oocytes is mixed with sperm chromatin. The half spindles that form subsequently fuse together. A more physiological method is to induce CSF arrested extracts to enter interphase by addition of calcium, whereupon the DNA replicates and kinetochores form. Addition of fresh CSF arrested extract then induces mitosis with centrosome duplication and spindle formation (for discussion of  
15 these systems see Tournebize and Heald, 1996).

Again, generally, candidate substances known to bind to a polypeptide of the invention, or non-functional polypeptide variants of the invention, would be tested in this assay. Alternatively, a high throughput assay may be used to identify modulators of spindle formation and function and the resulting identified substances tested for affects  
20 binding of the polypeptide of the invention as described above.

***Assays for DNA Replication***

Another assay to investigate the function of polypeptide of the invention and the effect of candidate substances on those functions is as assay for replication of DNA. A number of cell free systems have been developed to assay DNA replication. These can be  
25 used to assay the ability of a substance to prevent or inhibit DNA replication, by conducting the assay in the presence of the substance. Suitable cell-free assay systems include, for example the SV-40 assay (Li and Kelly, 1984, *Proc. Natl. Acad. Sci USA* 81, 6973-6977; Waga and Stillman, 1994, *Nature* 369, 207-212.). A *Drosophila* cell free replication system, for example as described by Crevel and Cotteril (1991), *EMBO J.* 10,

4361-4369, may also be used. A preferred assay is a cell free assay derived from *Xenopus* egg low speed supernatant extracts described in Blow and Laskey (1986, *Cell* 47,577-587) and Sheehan et al. (1988, *J. Cell Biol.* 106, 1-12), which measures the incorporation of nucleotides into a substrate consisting of *Xenopus* sperm DNA or HeLa nuclei. The nucleotides may be radiolabelled and incorporation assayed by scintillation counting. Alternatively and preferably, bromo-deoxy-uridine (BrdU) is used as a nucleotide substitute and replication activity measured by density substitution. The latter assay is able to distinguish genuine replication initiation events from incorporation as a result of DNA repair. The human cell-free replication assay reported by Krude, et al (1997), *Cell* 88, 109-19 may also be used to assay the effects of substances on the polypeptides of the invention.

#### ***Other In Vitro Assays***

Other assays for identifying substances that bind to a polypeptide of the invention are also provided. For example, substances which affect chromosome condensation may be assayed using the *in vitro* cell free system derived from *Xenopus* eggs, as known in the art.

Substances which affect kinase activity or proteolysis activity are of interest. It is known, for example, that temporal control of ubiquitin-proteasome mediated protein degradation is critical for normal G1 and S phase progression (reviewed in Krek 1998, *Curr Opin Genet Dev* 8, 36-42). A number of E3 ubiquitin protein ligases, designated SCFs (Skp1-cullin-F-box protein ligase complexes), confer substrate specificity on ubiquitination reactions, while protein kinases phosphorylate substrates destined for destruction and convert them into preferred targets for ubiquitin modification catalyzed by SCFs. Furthermore, ubiquitin-mediated proteolysis due to the anaphase-promoting complex/cyclosome (APC/C) is essential for separation of sister chromatids during mitosis, and exit from mitosis (Listovsky et al., 2000, *Exp Cell Res* 255, 184-191).

Substances which inhibit or affect kinase activity may be identified by means of a kinase assay as known in the art, for example, by measuring incorporation of <sup>32</sup>P into a suitable peptide or other substrate in the presence of the candidate substance. Similarly,

substances which inhibit or affect proteolytic activity may be assayed by detecting increased or decreased cleavage of suitable polypeptide substrates.

Assays for these and other protein or polypeptide activities are known to those skilled in the art, and may suitably be used to identify substances which bind to a polypeptide of the invention and affect its activity.

### ***Whole Cell Assays***

Candidate substances may also be tested on whole cells for their effect on cell cycle progression, including mitosis and/or meiosis. Preferably the candidate substances have been identified by the above-described *in vitro* methods. Alternatively, rapid throughput screens for substances capable of inhibiting cell division, typically mitosis, may be used as a preliminary screen and then used in the *in vitro* assay described above to confirm that the affect is on a particular polypeptide of the invention.

The candidate substance, i.e. the test compound, may be administered to the cell in several ways. For example, it may be added directly to the cell culture medium or injected into the cell. Alternatively, in the case of polypeptide candidate substances, the cell may be transfected with a nucleic acid construct which directs expression of the polypeptide in the cell. Preferably, the expression of the polypeptide is under the control of a regulatable promoter.

Typically, an assay to determine the effect of a candidate substance identified by the method of the invention on a particular stage of the cell division cycle comprises administering the candidate substance to a cell and determining whether the substance inhibits that stage of the cell division cycle. Techniques for measuring progress through the cell cycle in a cell population are well known in the art. The extent of progress through the cell cycle in treated cells is compared with the extent of progress through the cell cycle in an untreated control cell population to determine the degree of inhibition, if any. For example, an inhibitor of mitosis or meiosis may be assayed by measuring the proportion of cells in a population which are unable to undergo mitosis/meiosis and comparing this to the proportion of cells in an untreated population.

The concentration of candidate substances used will typically be such that the final concentration in the cells is similar to that described above for the *in vitro* assays.

A candidate substance is typically considered to be an inhibitor of a particular stage in the cell division cycle (for example, mitosis) if the proportion of cells undergoing that particular stage (i.e., mitosis) is reduced to below 50%, preferably below 40, 30, 20 or 10% of that observed in untreated control cell populations.

### THERAPEUTIC USES

Many tumours are associated with defects in cell cycle progression, for example loss of normal cell cycle control. Tumour cells may therefore exhibit rapid and often aberrant mitosis. One therapeutic approach to treating cancer may therefore be to inhibit mitosis in rapidly dividing cells. Such an approach may also be used for therapy of any proliferative disease in general. Thus, since the polypeptides of the invention appear to be required for normal cell cycle progression, they represent targets for inhibition of their functions, particularly in tumour cells and other proliferative cells.

The term proliferative disorder is used herein in a broad sense to include any disorder that requires control of the cell cycle, for example, cardiovascular disorders such as restenosis and cardiomyopathy, auto-immune disorders such as glomerulonephritis and rheumatoid arthritis, dermatological disorders such as psoriasis, anti-inflammatory, anti-fungal, antiparasitic disorders such as malaria, emphysema and alopecia.

One possible approach is to express anti-sense constructs directed against polynucleotides of the invention, preferably selectively in tumour cells, to inhibit gene function and prevent the tumour cell from progressing through the cell cycle. Anti-sense constructs may also be used to inhibit gene function to prevent cell cycle progression in a proliferative cell. Another approach is to use non-functional variants of polypeptides of the invention that compete with the endogenous gene product for cellular components of cell cycle machinery, resulting in inhibition of function. Alternatively, compounds identified by the assays described above as binding to a polypeptide of the invention may

be administered to tumour or proliferative cells to prevent the function of that polypeptide. This may be performed, for example, by means of gene therapy or by direct administration of the compounds. Suitable antibodies of the invention may also be used as therapeutic agents.

5           Alternatively, double-stranded (ds) RNA is a powerful way of interfering with gene expression in a range of organisms that has recently been shown to be successful in mammals (Wianny and Zernicka-Goetz, 2000, Nat Cell Biol 2000, 2, 70-75). Double stranded RNA corresponding to the sequence of a polynucleotide according to the invention can be introduced into or expressed in oocytes and cells of a candidate organism  
10 to interfere with cell division cycle progression.

          In addition, a number of the mutations described herein exhibit aberrant meiotic phenotypes. Aberrant meiosis is an important factor in infertility since mutations that affect only meiosis and not mitosis will lead to a viable organism but one that is unable to produce viable gametes and hence reproduce. Consequently, the elucidation of genes  
15 involved in meiosis is an important step in diagnosing and preventing/treating fertility problems. Thus the polypeptides of the invention identified in mutant *Drosophila* having meiotic defects (as is clearly indicated in the Examples) may be used in methods of identifying substances that affect meiosis. In addition, these polypeptides, and corresponding polynucleotides, may be used to study meiosis and identify possible  
20 mutations that are indicative of infertility. This will be of use in diagnosing infertility problems.

#### ADMINISTRATION

          Substances identified or identifiable by the assay methods of the invention may preferably be combined with various components to produce compositions of the  
25 invention. Preferably the compositions are combined with a pharmaceutically acceptable carrier or diluent to produce a pharmaceutical composition (which may be for human or animal use). Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. The composition of the invention may be administered by

direct injection. The composition may be formulated for parenteral, intramuscular, intravenous, subcutaneous, intraocular or transdermal administration. Typically, each protein may be administered at a dose of from 0.01 to 30 mg/kg body weight, preferably from 0.1 to 10 mg/kg, more preferably from 0.1 to 1 mg/kg body weight.

5 Polynucleotides/vectors encoding polypeptide components (or antisense constructs) for use in inhibiting cell cycle progression, for example, inhibiting mitosis or meiosis, may be administered directly as a naked nucleic acid construct. They may further comprise flanking sequences homologous to the host cell genome. When the polynucleotides/vectors are administered as a naked nucleic acid, the amount of nucleic  
10 acid administered may typically be in the range of from 1 µg to 10 mg, preferably from 100 µg to 1 mg. It is particularly preferred to use polynucleotides/ vectors that target specifically tumour or proliferative cells, for example by virtue of suitable regulatory constructs or by the use of targeted viral vectors.

Uptake of naked nucleic acid constructs by mammalian cells is enhanced by  
15 several known transfection techniques for example those including the use of transfection agents. Example of these agents include cationic agents (for example calcium phosphate and DEAE-dextran) and lipofectants (for example lipofectam<sup>TM</sup> and transfectam<sup>TM</sup>). Typically, nucleic acid constructs are mixed with the transfection agent to produce a composition.

20 Preferably the polynucleotide, polypeptide, compound or vector described here may be conjugated, joined, linked, fused, or otherwise associated with a membrane translocation sequence.

Preferably, the polynucleotide, polypeptide, compound or vector, etc described here may be delivered into cells by being conjugated with, joined to, linked to, fused to, or  
25 otherwise associated with a protein capable of crossing the plasma membrane and/or the nuclear membrane (i.e., a membrane translocation sequence). Preferably, the substance of interest is fused or conjugated to a domain or sequence from such a protein responsible for the translocational activity. Translocation domains and sequences for example include

domains and sequences from the HIV-1-trans-activating protein (Tat), *Drosophila* Antennapedia homeodomain protein and the herpes simplex-1 virus VP22 protein. In a highly preferred embodiment, the substance of interest is conjugated with penetratin protein or a fragment of this. Penetratin comprises the sequence

- 5 RQIKIWFQNRRMKWKK and is described in Derossi, *et al.*, (1994), *J. Biol. Chem.* 269, 10444-50; use of penetratin-drug conjugates for intracellular delivery is described in WO/00/01417. Truncated and modified forms of penetratin may also be used, as described in WO/00/29427.

- 10 Preferably the polynucleotide, polypeptide, compound or vector according to the invention is combined with a pharmaceutically acceptable carrier or diluent to produce a pharmaceutical composition. Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. The composition may be formulated for parenteral, intramuscular, intravenous, subcutaneous, intraocular or transdermal administration.

- 15 The routes of administration and dosages described are intended only as a guide since a skilled practitioner will be able to determine readily the optimum route of administration and dosage for any particular patient and condition.

- 20 The invention will now be further described by way of Examples, which are meant to serve to assist one of ordinary skill in the art in carrying out the invention and are not intended in any way to limit the scope of the invention.

**EXAMPLES****Generation and Identification of Lethal, Semi-Lethal and Sterile Third Chromosome Mutants Having Defects in Mitosis and/Or Meiosis, and Second Chromosome Mutants Having Defects in Imaginal Disc Development By P-Element****5 Insertion Mutagenesis*****P-element mutagenesis***

Transposable elements are widely used for mutagenesis in *Drosophila melanogaster* as they couple the advantages of providing effective genetic lesions with ease of detecting disrupted genes for the purpose of molecular cloning. To achieve near

10 saturation of the genome with mutations resulting from mobilisation of the P-lacW transposon (a P-element marked with a mini-white gene, bearing the *E.coli lacZ* gene as an enhancer trap, and an *E.coli* replicon and ampicillin resistance gene to facilitate ‘plasmid rescue’ of sequences at the site of the P-insertion), *Drosophila* females that are homozygous for *P-lacW* (inserted on the X chromosome) are crossed with males carrying

15 the transposase source P( $\Delta$ 2-3) (Deak et al., 1997). Random transpositions of the mutator element are then ‘captured’ in lines lacking transposase activity. Stable, or balanced, stocks bearing single lethal *P-lacW* insertions are made.

More than 41,000 lines are derived, of which approximately one-half are on the third chromosome. Originally some 3100 lethal or strong semi-lethal lines (in homozygous

20 conditions) are identified. During preliminary characterisation unstable lines and clusters of the same mutation event are eliminated leaving 2460 lines to be characterised.

***Screening for Mitotic and Meiotic Defects***

About half of the mutants in the collection are embryonic lethals. We have carried out cytological screens of the 1155 lines that comprise late larval lethals, pupal lethals,

25 pharate and adult semi-lethals for defective mitosis in the developing larval CNS. This has identified 69 mutations falling into 43 complementation groups that affect all stages of the mitotic cycle. The cytological screens involve examining orcein-stained squashed preparations of the larval CNS to detect abnormal mitotic cells. In lines where defects are

identified, the larval CNS is subjected to immunostaining to identify centromeres, spindle microtubules and DNA for further examination. This leads to clarification of the mitotic defect.

As a set of common functions are essential to both mitosis and meiosis, we then  
5 identify mutations resulting in sterility and failed progression through male meiosis. This involves examining squashed preparations larval, pupal or adult testes by phase contrast microscopy. We examine “onion stage” spermatids in the 519 pupal and pharate lethal lines and 463 adult “semi-lethal” and viable lines for variations in size and number of nuclei which provides an indication of whether there have been defects in either  
10 chromosome segregation or cytokinesis, respectively. A total of 54 lines of the 519 pupal and pharate lethal lines and 22 of the adult lines show such defects. However, another 67 lines show male sterility without having onion-stage defects. 12 lines showing onion stage defects have been scored as having mitotic defects in the independent cytological screen of squashed preparations of the larval CNS. Twelve further lines with onion stage defects  
15 show female sterility and of these, 10 show maternal effect mitotic defects in syncytial embryos. Thus greater than one half of the meiotic mutants scored appear to represent cell division functions specific to male meiosis or have targeted male germ-line specific enhancer elements, thus revealing their meiotic function but in this test not their mitotic function.

20 Further characterisation of testis preparations of each line by phase-contrast microscopy with and without staining with Hoechst to reveal DNA defined 6 broad categories of meiotic mutants:

8 mutants from the collection show defects in meiotic entry or at early stages in the first meiotic division (MF1-8).

25 18 mutants (15 complementation groups) show abnormal meiotic spindles (AB1-16). Mutants in this group almost invariably show an associated weak defect in cytokinesis, and 7 show a strong defect in spermatid differentiation. 3 of these mutants

also show mitotic defects in larval brains or in embryos derived from homozygous mutant mothers.

18 mutants (16 complementation groups) also show abnormal meiotic spindles that are strongly multipolar (MUL1-15). Three of these also show maternal effect mitotic abnormalities of multipolar spindles in syncytial embryos.

4 mutants (3 complementation groups) show strong defects at all stages of spermatogenesis from the pre-meiotic stages to spermatid elongation stages (PL1-3). In this respect they resemble the *polo<sup>1</sup>* mutation.

4 mutants show segregation defects as indicated by spermatid nuclei of heterogeneous sizes (SEG1-4). The spindles appear normal but all have what are either chromosome bridges or lagging chromosomes. One of these also shows a maternal effect.

9 mutants (7 complementation groups) show predominant cytokinesis defects. Two complementation groups also have cytokinesis defects in mitotic cells in the larval brain.

In the Examples below, the designations MF, AB, MUL, PL, SEG or CK are included in the category description where available. Further phenotype information for each mutant described in the results section is provided in the “Phenotype” field. There is considerable overlap between these categories, and it will be of much interest to distinguish between mutants in which the primary defect results in secondary consequences, and mutants that affect more than one aspect of spermatogenesis, as for example appears to be the case with *polo* mutants (Sunkel and Glover, 1988; Carmena et al, 1998).

In the Examples, lines exhibiting mitotic and meiotic phenotypes are categorised generally into four categories:

Category 1 : Failure to complete cytokinesis

Category 2 : Failure to enter M-phase

Category 3: Metaphase arrest

Category 4: Anaphase defect

Category 5: Small Imaginal Discs (Block to Proliferation; see below)

5           Category 1 phenotypes are exhibited by mutations in Examples 1 to 14; while Category 2 phenotypes are exhibited by mutations in Examples 15 to 19. Category 3 phenotypes are exhibited by mutations in Examples 20 to 30, Category 4 phenotypes are exhibited by mutations in Examples 31 to 53. Mutations in Examples 54 to 74 exhibit a Category 5 phenotype.

10           ***Generation and identification of second chromosome mutants having small or no imaginal discs.***

          In the case of the second chromosome the flies used were from a second chromosome P-element collection established in Szeged, Hungary (Torok et al., 1993). The process of P-element insertion mutagenesis is essentially as described above. 15475  
15       insertions were recovered, of which 2711 were lethal or semi-lethal. After elimination of clusters of identical mutants, 2399 lines representing 1748 independent lethal insertions were recovered. Lines were chosen from the second chromosome collection on the basis of having small or no imaginal discs, to indicate a disruption in cell cycle progression that leads to underdevelopment of the discs. All the second chromosome mutants referred to in  
20       the results section are noted under the "Phenotype" field as "second chromosome, small imaginal discs" and comprise Category 5.

***Cytological Mapping of the P-Element Insertion Sites***

          The site of insertion of the P-element in each mutant line was determined by *in situ* hybridisation of P-element DNA to salivary gland polytene chromosomes as described in  
25       Saunders et al., 1989. Wandering third stage larvae were dissected and fixed as described and incubated with biotin-labeled DNA made from the *P-lacW* plasmid. After signal

detection chromosomes were stained with Giemsa and examined by microscopy and signals indicating the presence of P elements were assigned to polytene chromosome bands referring to the Bridges map (Lefevre, 1976). In the majority of cases a single P element was detected, only 10% of lines having multiple (two or three) insertions. The site of insertion is given as the "Map Position" field in the results section (for example 77B)

### ***Plasmid Rescue of P-Elements from Mutant Drosophila Lines***

Genomic DNA was isolated from adult flies by the method of Jowett et al., 1986, and plasmid rescue from the genomic DNA was performed according to Pirrotta et al., 1986. This allows the recovery of genomic DNA adjacent to the P-element which facilitates the identification of the site of P-element insertion and of genes which may be disrupted by the insertion. Essentially, genomic DNA derived from about 200 flies was digested with a restriction enzyme known to have a site within the P-element (EcoR1 or SacII for cloning sequences to the left of the element, or XbaI, BglII, PstI or BamHI for sequences to the right of the element). The digested DNA was ligated overnight, and plasmids recovered by electroporation of the ligated DNA into *E.coli* XL1-blue competent cells. Appropriate primers from within the P-lacW sequence were used to determine the sequence of the genomic DNA flanking the element (on average, 400 bp of sequence were obtained). The rescue sequences are provided in the results section under the heading "Rescue sequence". Where more than one sequence was recovered, the orientation of each sequence is also given.

### ***Sequence Analysis of P Element Insertion Lines***

Sequences flanking the insertion site of the P-element were derived by P element rescue as described above. In some cases sequence was obtained from only one side of the insertion, while in other cases sequences were obtained from both sides of the insertion.

As a first step, each P element rescue sequence was used to search a total database of *Drosophila melanogaster* sequences (database of the Berkley *Drosophila* Genome project) using the BLASTN program (which compares a nucleic acid sequence with a nucleic acid database, (Altschul and Lipman 1990)) with default parameters.

The search may identify a number of different types of match including *Drosophila* ESTs, known *Drosophila* genes and cloned genomic regions.

The ability to identify genes already known to be essential for cell cycle progression using this approach was confirmed, in this example, by the rescue sequence  
5 obtained from line 1324/8 which mapped to the 77B locus which was used to search the database. A BLASTN search identified a number of matching *Drosophila* ESTs, a match with the known cell cycle regulatory gene *polo* and a cloned genomic region designated CSC: AC018188. These matches are recorded in the results sections under the field headings "*Drosophila* ESTs", "*Drosophila* gene hit" and "Genomic hit, Accession No.",  
10 respectively. Any entries under "*Drosophila* gene hit" are further annotated with "(BLASTN with Rescue sequence)" to show that the match was obtained using the rescue sequence rather than a *Drosophila* EST or genomic clone ORF (see below). Accession numbers of ESTs, genes and genomic clones are provided where known. Genomic clones designations often include the Genbank designation as part of a longer designation.  
15 However the Genbank designation is always the code beginning with "AC" and followed by six digits.

Where an EST was identified, this was subsequently used to search using the BLASTX program (default parameters) against databases of sequences from *Drosophila* and Homo sapiens (databases of the National centre for Biotechnology Information  
20 (NCBI), National Library of Medicine, National Institute of Health, USA). In the case of line 1104/16, the search identified a known human gene, phosphatidylinositol transfer protein (accession no. P48739) implying a novel function for this protein in cytokinesis. Human Homologues identified as a result of a BLASTX search using a *Drosophila* EST are shown in the results section under the heading "Human homologues" and annotated  
25 with "(BLASTX with EST)". *Drosophila* genes identified as a result of a BLASTX search using a *Drosophila* EST are shown in the results section under the heading "*Drosophila* gene hit" and annotated with "(BLASTX with EST)".

Where no *Drosophila* gene was identified using the initial BLASTN search but a matching genomic clone was found (a Bac or P1 clone often in excess of 100 kilobases), a

20 kilobase segment of this genomic sequence (10 kilobases either side flanking the site of the P-element insertion) was subjected to a number of analyses.

If the rescue sequence matched sequences that lie within a known gene present within the genomic clone then these are presented under the heading “*Drosophila* gene hit  
5 (BLASTN with Rescue sequence”. The known gene sequence was then used in a BLASTX search of a human database (NCBI – see above) to identify any human homologues. These are shown in the “Human homologue” field and annotated with “(BLASTX with *Drosophila* gene)”.

If the rescue sequence does not match any sequences that lie with a known gene  
10 within the genomic clone then the occurrence of ORFs within the 20 kilobase genomic segment was predicted using the Genscan programme (Burge and Karlin, 1997). Where the P-element was observed to be inserted into the coding region or within the 5’ untranslated region (which we defined as within 2 kilobases of the predicted start of the coding region) we assume the P element to be capable of disrupting the expression of the  
15 predicted gene. Each predicted open reading frame (or predicted coding sequence) was then used to search *Drosophila* and human databases using the TBLASTN program (compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames) and/or the TBLASTX program (compares a nucleotide query sequence dynamically translated in all reading frames against a nucleotide sequence  
20 database dynamically translated in all reading frames) to determine whether the predicted open reading frame corresponded to a known gene. Typically, TBLASTX is only used when no matches are found using TBLASTN.

Where the TBLASTN search found a known *Drosophila* gene, then this is indicated in the results in the “*Drosophila* gene hit” field, annotated with “(TBLASTN  
25 with predicted ORF)”. The *Drosophila* gene sequence was then typically used to search a human database (NCBI – see above) to identify any human homologues using BLASTX. These are shown in the “Human homologue” field and annotated with “(BLASTX with *Drosophila* gene)”.

Where the TBLASTN and/or TBLASTX search found a known human gene, then this is indicated in the results in the “Human homologue” field, annotated with “(TBLASTN (or TBLASTX) with predicted ORF)”.

If the TBLASTN and/or TBLASTX search found no *Drosophila* or human genes, then it was assumed that the original ORF corresponds to a novel gene. If the TBLASTN search found no *Drosophila* genes but identified a human homologue, then it was assumed that the original ORF corresponds to a novel *Drosophila* homologue of a known human gene.

***Additional Sequence Analysis using the Annotated D. melanogaster Sequence (GadFly).***

Rescue sequences were also used to search the fully annotated version of the *Drosophila* genome (GadFly; Adams, et al., 2000, Science 287, 2185-2195), using GlyBLAST at the Berkeley *Drosophila* Genome Projects web site to identify the genome segment (usually approximately 200-250 kb) containing the P-element insertion site. The graphic representation of the genomic fragment available at GadFly allows the identification of all real and theoretical genes which flank the site of insertion. Candidate genes where the P-element is either inserted within the gene or close to the 5' end of the gene were identified. In GadFly, the *Drosophila* genes are given the designation CG (Complete gene) and usually details of human homologues are also given. In most cases, this data confirms the data derived from the sequence analysis procedure described above, and in some cases new data is obtained. Where available both sets of data are included in the individual Examples described below. To identify further candidate human homologues, BLASTP (amino acid query sequence against amino acid database) searches with *Drosophila* sequences are used against the human genome project database and also the Ensembl dataset. The Ensembl dataset comprises GeneWise gene predictions using a protein template where possible or Genscan followed by BLAST confirmation via protein, cDNA or EST hits. These are matched using WUBLASTP with default parameters (Altschul et al., 1990, *J Mol Biol* 215, 403-10). The results are filtered to contain only potential homologues. Only matches with the identity of more than 50% and length of more than 50 amino acids are included.

***Confirmation of Cell Cycle Involvement of Candidate Genes Using Double Stranded RNA Interference (RNAi)***

P-elements usually insert into the region 5' to a *Drosophila* gene. This means that there is sometimes more than one candidate gene affected, as the P-element can insert into the 5' regions of two diverging genes (one on each DNA strand). In order to confirm which of the candidate genes is responsible for the cell cycle phenotype observed in the fly line, we use the technique of double stranded RNA interference to specifically knock out gene expression in *Drosophila* cells in tissue culture (Clemens, et al., 2000, *Proc. Natl. Acad. Sci. USA*, 6499-6503). The overall strategy is to prepare double stranded RNA (dsRNA) specific to each gene of interest and to transfect this into Schneider's *Drosophila* line 2 to inhibit the expression of the particular gene. The dsRNA is prepared from a double stranded, gene specific PCR product with a T7 RNA polymerase binding site at each end. The PCR primers consist of 25-30 bases of gene specific sequence fused to a T7 polymerase binding site (TAATACGACTCACTATAGGACA), and are designed to amplify a DNA fragment of around 500bp. Although this is the optimal size, the sequences in fact range from 450 bp to 650 bp. Where possible, PCR amplification is performed using genomic DNA purified from Schneider's *Drosophila* line 2 as a template. This is only feasible where the gene has an exon of 450 bp or more. In instances where the gene possesses only short exons of less than 450 bp, primers are designed in different exons and PCR amplification is performed using cDNA derived from Schneider's *Drosophila* line 2 as a template.

A sample of PCR product is analysed by horizontal gel electrophoresis and the DNA purified using a Qiagen QiaQuick PCR purification kit. 1µg of DNA is used as the template in the preparation of gene specific single stranded RNA using the Ambion T7 Megascript kit. Single stranded RNA is produced from both strands of the template and is purified and immediately annealed by heating to 90 degrees C for 15 mins followed by gradual cooling to room temperature overnight. A sample of the dsRNA is analysed by horizontal gel electrophoresis.

3µg of dsRNA is transfected into Schneider's *Drosophila* line 2 using the transfection agent, Transfect (Gibco) and the cells incubated for 72 hours prior to fixation.

The DNA content of the cells is analysed by staining with propidium iodide and standard FACS analysis for DNA content. The cells in G1 and G2/S phases of the cell cycle are visualised as two separate population peaks in normal cycling S2 cells. In each experiment, Red Fluorescent Protein dsRNA is used as a negative control. In some cases the phenotype is confirmed by fixing cells on poly-lysine covered slides which are then stained for DNA using DAPI and for tubulin using an anti-tubulin antibody YL1/2 and appropriate fluorescent secondary antibody to visualise aberrant mitoses.

It should be noted that RNAi could not confirm phenotype in all cases. This is to be expected as the method relies on the ability of dsRNA to prevent new protein expression. Consequently, it is necessary that S2 cells express the specific cDNA of the gene in question, and also that the protein is turned over rapidly. It would therefore probably be difficult to sufficiently reduce levels of very stable proteins using this approach.

The layout of a typical entry in the results section is shown below. Not all fields present in the actual results section contain information for each individual *Drosophila* line described.

#### TYPICAL RESULTS LAYOUT

20	<b>Line ID</b> - <i>Drosophila</i> line designation <b>Category</b> - Description of phenotype <b>Reversion</b> - R = revertant, NR = non revertant, ? = not determined <b>Map Position</b> - according to the Bridges map (Lefevre, 1976).
----	--

25	<b>Rescue ID</b> <b>Rescue Sequence</b> [nucleotide sequence]
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#### Genomic hit, Accession No.

30	<b>Associated ORF</b> GENSCAN_predicted_peptide [results of Genscan - amino acid sequence] GENSCAN_predicted_CDS [results of Genscan nucleotide sequence]
----	---

35	<b><i>Drosophila</i> Gene Hit</b> (BLASTN with rescue sequence)
----	--

(TBLASTN (or TBLASTX) with predicted ORF)  
(BLASTX with EST)

### Human Homologue

- 5 (BLASTX with *Drosophila* gene)  
(TBLASTN (or TBLASTX) with predicted ORF)  
(BLASTX with EST)

### *Drosophila* EST

- 10 **Annotated *Drosophila* genome genomic segment**  
**Annotated *Drosophila* genome Complete gene candidate**  
**Human homologue of Complete gene candidate**

**Putative function** Derived from homologies or *Drosophila* experimental data

- 15 **Confirmation by RNAi** Description of Facs analysis DNA content profile

A specific example is as follows:

- 20 **Line ID** 1324/8  
**Category** Mitotic defects in brain: metaphase arrest  
(overcondensation, some circular chromosomes, no anaphases,  
very high mitotic index, metaphase (or less aligned) with bipolar  
25 spindle, no CP190 staining)  
**Reversion** R  
**Map Position** 77B  
**Rescue ID** B1E  
30 **Rescue Sequence**  
GTTTTGCCCATCGATTGCACGAAAACCAAGCACAAAGCGGAGAACGCGCCGA  
AACCGTTTCGATTTTTTAAATGCCAAAATGAATTGGACGTGAAGCGTCAGCTGA  
ATTGGTGTGCCCGTTTCGGTGGCTATCGCACACTTTCTGGTATTTATCGCGGTA  
TTTTGTTGAGTGTTGAACAACAAATTCTATGGCCGTTACCCTTTTGAATTTACT  
35 TACTGGCGTTTACTCTGTTCGAATTGAGCGCAATATTTTTTCCTATTGCTCTGC  
GCAACACTGTGTTTTAACCGCTATTTATTTGAAAATCTACAAAACTAACCGTT  
TACATTTTTGAAATTTCCAAAAGGGTTTTCCATAAATTGAGTTTTACTAAAACC  
AGTCCAACGGTCCAACCTTTATATTGTTAGAAGCCCCTTTTCCTAATTTGAATTG  
GCTTGCAAACGTTTTTCCTGAATTTAAAAATACTGCCACCCTTGTTAATTGCAGG  
40 TTTTCCGAATCCCTGATTTGTTGTTTTAAAAAGAAAATTTATTAGAAACAGCTA  
TCTCAACC

**Genomic hit, Accession No.** CSC:AC018188

***Drosophila* Gene Hit** Polo (X63361)

- 45 **Human Homologue** BLASTX PLK-1 (P53350)

***Drosophila* EST** several including LD11851 (AA392613) which match polo

**Annotated *Drosophila* genome genomic segment** AE003514

**Annotated *Drosophila* genome Complete gene candidate** CG12306

**Human homolog of Complete gene candidate**

1e-169 1709658 P53350

PLK1\_HUMAN

SERINE/THREONINE-  
PROTEIN KINASE PLK  
(PLK-1)

5

**Putative function**

Serine/threonine kinase known to be required for mitosis

10

**Confirmation by RNAi**

Reduced G1 and G2/M peaks indicating fewer cycling cells, microscopy analysis of DNA and tubulin staining identified monopolar spindles characteristic of polo mutation in *Drosophila*.

**CATEGORY 1: FAILURE TO COMPLETE CYTOKINESIS****Example 1 (Category 1)**

**Line ID** 1031/14  
**Category** Mitotic defects in brain: cytokinesis defect (polyploidy)  
**Reversion** R  
**Map Position** 74B

**Rescue ID** 2A3B  
**Rescue Sequence 1**  
 CCCCAGAACATATGTTTCAGTGTGGCCGCAGCAGAGTTGTCAAAACACGCTCCC  
 CAATGAAATAACCTAAATGTGCCATCACTGTTACTTAACAGTTTCTGTTACTTT  
 TCTAGCGGCATGTCAAAAAAACAAAAATATAGAAAATGCTAAATATATATTG  
 15 GACTAATGTGTTTAAATGTAACCTTACACTAGTAACAGATCCCCATTAATAAAA  
 GCCAAACTCTAAAATTCTGCCACAAGTACTATTTCTCACGTAACACCTTACTA  
 ACGGATTTACATGATATCTACGACAAGAACTGTTTGCTGATATAAAATTGC  
 TATCACCCTTTCCGTAAACACTTTTACACTGATGGATTACAAGTTCAATTAAT  
 ACATCAACTTACCTTAACAATTTTAAGACAATAACACTCCCACAATTTAATT  
 20 CAACCTACACCGCTTGATAATCAGCTGTTCTGTACAAAAACAATAACACTGT  
 TAACAACAGCGCACAGTGGATAATACAGTCCTAAAGGCAATATACCCATTG  
 GCATTTTT

**Rescue ID** 2A3S  
**Rescue Sequence 2**  
 TTCCGGGGAGAATGGCTGCGATTTTCGCGTCGGTAAAAATAGCAAATACTCGTTA  
 ATGTGCTGTGGGAACGCTTCCTCCCCGGCCCCAAAGTGGCCCCGAAGAAAGTGA  
 GCAAATGTGCGCGCCGCAAGATAGTCGCCGCGCAACAAACGATAGTGACGAAA  
 GTGATTTAATTCAACTACCAGCACTCCCGCAAATACGATGAGTATGTGCGCGCG  
 30 CGGCAACACAACCTCTGGACTTGCAGCCGCTCCTGGCGGAGAGCGATGTGCGGAA  
 ACAGGGAGCTGGAGGAGAAGATGGGCGGATCGGCGGATCGGTCATCGCTGCTC  
 GATGGATCCGGTTCGAAGGAGCTGAGTCACCGGGAACGCGAGGACTCGGCGTT  
 GTTCGTCAAGAAGATCGGGAGCGCCTTGTTCTATGGCTTGTCTCCTTCATGATT  
 ACGGTGGTAAACAAGACGGTGCTTACCTCCTACCACTTCCCCTCGTTCCTGTTCC  
 35 TCAGCCTCGGGCAACTTACTGCTAGCATTGTGGTCCTGGGCATGGGCAAAGCGC  
 CTGAAAATGGTGAACCTTTTCCCCTTTTGCAGAGGAATACCTTCGCCAAGATCTTT  
 CCGCTGCCACTGATATTTCTGGGAAACATGATGTTTGGACTGGGTGGCACAAAA  
 ACCTTGAGTCTGCCCATGTTTCGCAGCCCTACGAC

**Genomic hit, Accession No.** AC019515

**Associated ORF**

Genscan ORF1 predicted sequences:>15:31:57|GENSCAN\_predicted\_peptide\_4|373\_aa

MSMSRGGNTTLDLQPLLAESDVGNRELEEKMGGSADRSSLDDGSGSKELSHRER  
 EDSALFVKKIGSALFYGLSSFMITVVNKT VLT SYHFPSFLFSLGQLTASIVVLGMG  
 KRLKLVNFPPLQRNTFAKIFPLPLIFLGNMMFGLGGTKTSLPMFAALRRFSILMT  
 MLELEKILGLRPSNAVQVS VYAMIGGALLAASDDL SFNMRGYIYVMITNALTASN  
 5 GVVYVKKKLDTSEIGKYGLMYNSLFMFLPALALNYVTGNLDQALNFEQWNSV  
 FVVQFLLSCVMGFILSYSTILCTQFNSALTTTIVGCLKNICVTYLGMFIGGDYVFSW  
 LNCIGINISVLASLLYTYVTFRRKRAPDKQDHL PSTRGENV

>15:31:57|GENSCAN\_predicted\_CDS\_4|1122\_bp

10 atgagtatgtcgcggcggaacacaactctggacttcagccgctcctggcggagagcgcgatgtcgaaacagggagctgga  
 ggagaagatggcgggatcgcgatcggtcatcgtcgcgatggatccggttcgaaggagctgagtcaccgggaacgcgag  
 gactcggcggtgttcgtcaagaagatcgggagcgccgtgttatggctgtcctcctcatgattacgggtgtaacaagacgggtgc  
 ttacctctaccacttcccctcgttctgttctcagcctcgggcaacttactgctagcattgtggtcctggcgcggaagcgcct  
 gaaattggtgaacttccccctctgcagaggaataccttcgcaagatcttccgctgccactgatattctgggaaacatgatgttg  
 15 gactgggtggcacaacaccttgagctgcccgtgttcgagccctacgacgcttctctatctgatgacctgctggtgagctca  
 agatcctgggactgcgaccttcgaatgcggttcaggtcagcgatacgaatgatcggtggagcgcgtgctggccgctctgatga  
 tctgtcctcaacatgaggggctacatctatgtgatgactaacgacctgaccgctcgaatggcgatatgtgaagaaaaactc  
 gacacctcgagatcggaagtagcgccatgtactacaactcgcgtgttatgtttctgcctgcctggccctcaactatgttacag  
 ggaatctagatcaggcgctgaacttgaacaatggaatgactcagtggttggtgcagttcctgctcagttgcgttatgggtttcatc  
 20 ctatcgtacagcaccatcctgtgcacgaattcaactcggcgctgaccaccaccattgtgggatgcctgaaaacatctgcgtaac  
 atatctgggcatgttcattggaggcgactacgtctctcgtggctcaactgtattgggatcaacatcagcgtgctggctagtctgctc  
 acacgtacgtcacttttcggcggaagcgggctcccgataagcaggaccactgcccagcaccgcggcgagaatgtctag

25 **Human Homologue** (TBLASTN with ORF1): KIAA0260 gene (D87449) and putative  
 Sqv-7-like protein (AJ005866)  
**Drosophila EST** CK00510 (AA140776)

**Annotated Drosophila genome genomic segment** AE003524  
**Annotated Drosophila genome Complete gene candidate** CG3874 – novel glucose-6-  
 30 phosphate transporter

**Human homologue of Complete gene candidate** EMBL:D87449 protein  
 KIAA0260\_id:BAA13390  
 gi:166578 Similar to a  
 35 C.elegans protein encoded in  
 cosmid C52E12 (U50135) and  
 Ensembl predicted gene  
 ENSG00000024527  
 Clone:AL133320  
 40 Contig:AL133320.00001  
 8.10E-95

**Putative function** Sugar modification protein similar to proteins involved in  
 Drosophila cytokinesis and signalling

45 **Confirmation by RNAi** Marked increased G1 and S peak indicating mainly arrest in  
 G1

**Example 2 (Category 1)**

**Line ID** 1066/5  
**Category** Male semi-sterile, Meiotic defects in testis: cytokinesis defects, segregation defects.  
 5 (Seg-01/62)  
**Reversion** ?  
**Map Position** 89B  
 10 **Rescue ID** F9E  
**Rescue Sequence**  
 GTATACCATTAGAGAATATGATGAAGAAGGACTGTAAGAAGATCCTTCAGTG  
 AATTTGACTGCTGACGTCGATCGGAACCTTGCTGCGCTGACGTACAAAATCGCG  
 AAGTGAATAAATAATATGGATGAGACCCTGTTTCGCCGACATATACAATAGTG  
 15 CTCAAGACCTAATGGAATTATACGTTAATAACCAGCCACATTTCTTAGATATTT  
 CTAATATGAGCCATCTGCTGCAGGTTCTTTCCAATATCTAATTCTAGATCTTCT  
 TCGAATACGACCTTTTTGGCCATGAAACGATGATTTGCCACTTCATTCAACAG  
 CATTAATTTGTCATGATTCTCTTAAGCGTGCACTTTATCTGAAAGTCTGAACAG  
 CTGGCTGCGAAATGGATCCCCGGGATTGGAGATGGCAAGTAAATCTGTCCTCG  
 20 CTACAAACAAGTGGGCACCACTGGGCATTCGGGGAATAGGGATATGGGTTGG  
 GAATGGGGATATATTGTGGCATTGGCGAAAGGTCGCTATGC

**Genomic hit, Accession No.** CSC:AC019750

25 **Associated ORF**  
 >16:04:57|GENSCAN\_predicted\_peptide\_4|418\_aa  
 MKPIPNESKGTLLAAVGDA TVVH D VCTLFAVELDPYLRSSMGMRTTRRAQSGALLL  
 QLLAVADGGFAAHICACKCRLRLPHVTCCNRNPFKATAKAKGQAVSSTKPNQL  
 CFHGCCGWITTKGETFTENSPSIMSGFAWERHSLGECVVVAGTEQILLIGRTLIGR  
 30 MSHTQTDSTSPFVVDCHSQLCGSKCKCICVSVGFCVRPSCQRFDMKIVWANLAM  
 QKRFLLGAAIADMCCRNSVIWCKLQLDPVKPIDERADGSGLALVTKVCDNNNIV  
 HYVVVAGVTGSQSRSLQPLRSGQNESTEQWPRTKGEGGFNNNSRNNKHSAPT  
 QEQQELWQKQLLQDQRDDCHASGSFQSASFAETRSFTFDDTTAHSEFCFRTRA EK  
 RRILVLLET SIKLKPDKYATSGHTRRCAIGLLHSII  
 35 >16:04:57|GENSCAN\_predicted\_CDS\_4|1257\_bp  
 atgaaacccattccaacgaatccaagggaaacccttgccgcagttggagatgctactgtgtcatgacgtgtgtactttgttgcg  
 tagagcttgatccctatctcaggagcagcatgggaatgaggacgcgtagagctcaaagcggcgctctgttattacagctccttgcg  
 gttgccgatggaggtttgtgctcatattgtgcctgcaagtgtcggcttcgttgccacatgtcacatgttgctgcaaccggaatcct  
 40 ttcaaggcaactgcaaaagcaaaaggtcagggcgtcagctccactaaaccaaccagctttgctttcacggctgctgtgctggat  
 aattactaccaaaaggtgaaacgttcaccgaaaactgcacgcatcatgagcgggtttgctgggagcggcatagccttggtgagt  
 gcgtggttggtggaacggaacaaatcctgctgattggcaggacattgattggccgatgagccatactcaaactgattcgacc  
 agcccctttgtgactgtcactgcgaactgtcggctccaagtcaaatgtatctgttatctgtaggtttctgtgtgcgccgtct  
 tgtcagcgctttgacatgaaaatagtttggccaacttgctatgcaaaagcgatttctattaggagccgccatgcgcacatgtgct  
 45 gccgaaattcggtgatttgggtgcaaaactgcagctagatccagtcgaagcaattgacgaaagagccgacggcagcggtcttgact  
 ggttaccaaagtatgcgataacaataacatcgccactatgtggctgtgtggtgggttacgggcagtcagtcacgggtcacggctgc

60

aaccctccgctccggccaaaacgagtcacagaacaatggccaaggacgaaggggggggaggggggattcaataacaaca  
gcaggaacaacaacattctgctcccacgcaagagcagcaggaactgtggcaaaaacagctgctgcaggatcaacgagacgat  
tgcatgccagtgaagctccagtctgcgtcattcgcggagacgcgtagttcacgttcacgacacaaccgctcacagcgaattt  
tgtttcggactagagctgagaaacggcgaaatttggtgcttctggaacatcgattaaactaaaacccgataagtatgcgacaagc  
5 ggtcacactcggcgatgtgcgataggattgtgcattcgattatag

***Drosophila* Gene Hit** rescue sequence: mitotic heterochromatin fragment clone CH(2)6  
(L36595) and subtelomeric heterochromatin repeats (L03284).

10 **Human Homologue** TBLASTN with ORF1: nebula (nla) (AF147700)  
BLASTX with nebula: Down Syndrome candidate region 1-like  
protein 2 (AF176117)

***Drosophila* EST** rescue sequence: CK01138 (AA141069)

15 **Annotated *Drosophila* genome genomic segment** AE003712  
**Annotated *Drosophila* genome Complete gene candidate** CG6072 - nebula  
CG6046 – sap18

20 **Human homologue of Complete gene candidate** CG6072- 8e-36 'ZAKI4 a thyroid  
hormone responsive gene in human  
skin fibroblasts' also known as  
DOWN SYNDROME CANDIDATE  
REGION 1-LIKE 1; DSCR1L1  
EMBL:D83407  
25 protein\_id:BAA11911 gi:143504

30 CG6046- 3e-45 2108210 (U96915)  
sin3 associated polypeptide p18  
[Homo sapiens] and gi5032067  
C7E479FFE9CA5774  
[ref|NP\_005861.1| sin3-associated  
polypeptide, 18kD [Homo sapiens]  
(1.90E-43)

35 **Putative function** Nebula unknown function, Sap18 transcription factor

**Confirmation by RNAi** Both show reduction in G1 and G2/S peaks indicating fewer  
cycling cells

40

**Line ID** 234/50  
**Category** Meiotic defects in testis: cytokinesis defects, abnormal spindles.  
(Ab-02/12)  
**Reversion** R  
5 **Map Position** 89B

**Rescue ID** 2C5E

**Rescue Sequence**

10 GTTTGACTGCTGACGTCGATCGGAACTTGCTGCGCTGACGTACAAAATCGCGA  
AGTGAATAAATAATATGGATGAGACTCCTGTTTCGCCGACATATACAATAGTG  
CTCAAGACCCTAATGGAATTATACGTTAATAACCAGCCACATTTCTTAGATAT  
TTCTAATATGAGCCATCTGCTGCAGGTTCTTTCCAATATCTAATTCTAGATCTT  
CTTCGAATACGACCTTTTTGGCCATGAAACGATGATTTGCCACTTCATTCACAA  
GCATTAATTTGTCATGATTCTCTTAAGCGTGCACCTTATCTGAAAGTCTGAACA  
15 GCTGGCTGCGAAATGGATTCCCCGGATTGGAGATGGCAAGTAAATCTGTCCTC  
GCTACAAACAAGTGGGCACCACTGGGCATTTCGGGGAATAGGGATATGGGTTG  
GAAA

**Drosophila EST** rescue sequence: CK01138 (AA141069)

20 All other entries as for 1066/5.

**Example 3 (Category 1)**

**Line ID** 1104/16  
**Category** Mitotic defects in brain: cytokinesis defect  
 5 (no overcondensation of diploids, high polyploidy)  
**Reversion** R  
**Map Position** 92A

**Rescue ID** B5P

10 **Rescue Sequence 1**

CTCCGGACACGCAGTAGCTAAATAACAACTCATTACTAGTATATTACTGCCG  
 CCGATTTGCAAGCGCGTACCGATCCCGATAACCAGGCCAATCGCACTCCCCAGT  
 TGTACGTCATCACTTAAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATT  
 GATATTCCGCCCGCTGTGTGTGCGTGTGTATTGCAAGAGAGTGTGTGTGTGT  
 15 GTGTGCATATGACTCGTGCCTTAGCCGACAATTGGAGAAAAAGCATTACCAA  
 TCCCAATTGGCTAACTAACTAAAGTTGGCTTGGCCAAACATAAACAAAAAGT  
 GCGGGCGCAGCGATTTGGCAGCGAAACATATACACCAAAGCGCTATTGGCAG  
 ATATATATGTAGATTAAATATAGAAAGTGCGTGCGAAGGTTAAGAGTCGAGT  
 GCAAGTGCATTTATATTTGGAAATAATAAATGCTACAAT

20

**Rescue ID** B5E

**Rescue Sequence 2**

GTCCGGAGCGGAGCTAAAGTTTCGATGTTTCGTGCAAAACACTTCGATTCCGATA  
 GGCGGATGCTATCGATTTCGGCGATGCCCGTTGGTCACACTTGGTGGTGGGCG  
 25 CTGCCCGTCGCCGACTATCGATAGCACAAAGCGGGTTATTTAGGTGTGCGCAGC  
 TTGTAAGGGTGACTCATGCTGTTAAAATTATTATAAAAAGTTAATGAATATAA  
 TATAGTTATAATAAAATTATATATAAATCTATAAGATCAAAGATCATCAGTTA  
 TCATTTATCATTTGATTATATGAAAAACAAGAACAGAAACAAGATTTAATAGG  
 TTTTGTAAATGTGAAAATGTGGGTACCCCCAATTCTTATTCGAAATTAAATAA  
 30 CCTAAAGAACAGTTATACACAGATAGGTAATTTGCACATAAGCCAAATTTTGT  
 CTAGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCCGTGATACGCC  
 TATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTA

**Genomic hit, Accession No.** AC006589

35 **Associated ORF**

Genscan: ORF1 predicted sequences

>/tmp/aaaaainga|GENSCAN\_predicted\_peptide\_2|850\_aa

MATRGANVIWFRHGLRLHDNPALLAALADKDQGIALIPVFIFDGESAGTKNVGY  
 NMRFLDLSLQDIDDQLQAATDGRGRLLVFEGEPAYIFRRLHEQVRLHRICIEQDC  
 40 EPIWNERDESIRSLCRELNIDFVEKVSHTLWDPQLVIETNGGIPPLTYQMFLIRCTH  
 HNGDVNGDEDTGEGEGTGGRIDWAKEGACWRAGNSDEQECQACQSVSSVIMM  
 VLQYSNNPAHHCQLECLMTLKHNVVKDILCVVAYGTAVSRTSAAKLLFYYP  
 AFNANLFDKRVLLSKLTNDLVPFTCQREHCPNSGNAEAAKVCYDHSISIAYPDC  
 PPPLYLCIECANEIHRHGSLEFGDILHPMQQVSMVCENKNCRSNEKSAFSICFSTE  
 45 CASFNGNHPIRYCSQCHSNRHSRRGGDHVVHRS LQPAWQMDPEMQMHMVESV  
 VSLLREAKPLNFEPGKESSSSSESKKNGSGITADNISLEERQRLGRYGIWLLVGRCTP

TADTPVEVLGRILSMLFHWFWHTA YSYDGFISCLVPHPEYARVGGHWETLASRT  
 SHLKEGLQRLICLVPEVITSEIWDYVMPHWMEAITNDVAEKELNELKIVLSKILD  
 PEMSPLGFD AKTMYNFVAIRFEKTTAKVQQQALHWLQILTKLEILPLVQLFAMF  
 GDGVRIMKYGIQHELMREKDAQS QSLAKAPKTPCKESKETKADMANPPRPPVVE  
 5 DDSGNTSAISDDEAPTNRHTEFSTDAEHNLTCCILMLDILLKQMELODVEQHMGI  
 HTSVCENVSRLIKCMVTAARVGLSSHVCALKVPIDIEEEKSSRKSPPESDKEKTR  
 DRDVSLSMAPLPIPLGLGGFADP

>/tmp/aaaaainga|GENSCAN\_predicted\_CDS\_2|2553\_bp

10 atggccacgcgagggcggaatgtgattggttcgccatggattgcgcctccatgataat  
 cccgctctattggccgccctcgccgataaggatcagggtatagccctaattcccgtttcatattcgaaggagagagtgcagggtacc  
 aagaatgtgggttacaatcggatgcgtttcctcctggactcgttcaggacatcgatgcagctacaggcggaactgatggacg  
 tggacgcctcctggtcttcgagggcgaaacggccttatcttcgccggctacatgagcaagtgcgtctgcacaggattgcatag  
 agcaggactgcgagccaatttggatgagcgcgatgaaagcatccgttctctatgtcgggagctgaatatgcactttgtcgagaag  
 15 gtatcacacacgctttgggatccgaattggtgattgagaccaatggtggcattccaccgctgacctaccaaatgttcctgatacgt  
 gcacgcaccacaatggagatgtgaatggggatgaggatacgggagagaagggaacggcggaaggatcgactgggcta  
 aggaaggggcctgttggaggcgggaaactccgacgaacagggaatgtcaggcctgccaatcagtgctcctcggtcatcatgatg  
 gtgctccagtactccaacaatccagcgcacatcattgccagctcctggagtgctgctgactcctaagcacaatgtcgtcaaggacatc  
 ctctgcgtgtggcatacggaaacgctgtttcccgacctcggctgccaagctgctcttctactactggccagccttaacgccaatc  
 20 tgttcgatcgaaagtctactctccaaactaaccaatgacctagtgccttcacctgccaacgggagcactgtccgaactccggg  
 aatggggaggcagcaagggtgtgctacgaccacagcattagcatcgatacgcgccgattgtccaccgcccctttacctgtgca  
 tcgagtgcgccaacgagattcatcgggagcagcgaagcctggagtgcgcgacattctgcatcccatgcagcaggatcatgatgg  
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 catccgatccgctactgcagccagtccacagtaataggcacaattcccggcgagggtggcgatcacgtggtccatcgagctctgc  
 25 agcccgctggcagatggatccagagatgcagatgcacatgggtggagtcgggtgtaagccttctgcgagaggcggaagccacta  
 aactttgagcccggaaggagctctcgtcgtccgagtcacaaaagaacggctccggcatcacagctgacaatatttctctggagg  
 aacgccagagactgggacgctatggtatctggtactggtgggtcgctgtacaccactgcagatactccgtagaagtctggg  
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 30 gtgccatagagggttatcacttccgaaattgggactatgtgatccgcactggatggaggccatcaccaacgacgtggccgaga  
 aggaactgaacgagctgaagattgtgctcagcaagatcctcgatccggaatgtcgctctgggctttgatccaaaacctgtac  
 aactttgtggccattcgatttgagaagacaacggcaagggtgcagcagcaggcactccactggctgcagatcctcaccaagctgg  
 agattctcattccactgggtccagtgttcgccatgttcggcgatggtgttcgcataatgaaatacggcatccagcagcagctgatgcg  
 cgagaaggatgcccaatctcagtcctggccaaggctcccaagaccccggtgtaagagagcaaggagaccaaagcggtatg  
 35 gccaatccgcccaggcctcctgttgcgaggatgactctgtaatacgtctgccatttcggatgacgaggcgccacgaatcgta  
 cacggaattctccacggatgctgagcacaatctacctgttgcatcctcatgctggacatacttgaagcaaatggaactacagga  
 cgtggagcagcacatgggcatccatacgaagtgtcgcgagaacgltccaggctgatcaagtgcagtggtcactgcagctcagat  
 gggtctcagtagtcatgtctgcgcctaaagggtcccatcaggacatcattgaggaagaaaagtcctcgcgcaatctccaccg  
 aatccgacaaggaaaagaccggtgatcgagatgttccctctcgatggctccactaccattccgctgggacctttaggaggattg  
 40 cagacccttaa

**Human Homologue** BLASTX with EST: Phosphatidylinositol transfer protein  
 (P48739)

45 **Drosophila EST** SD01527 (AI530804), GH18602 (AI387906)

**Annotated Drosophila genome genomic segment** AE003725

**Annotated *Drosophila* genome Complete gene candidate** CG5269 – vib PIP transfer protein

5      **Human homologue of Complete gene candidate**    1e-90 1346772 P48739  
PPI2\_HUMAN  
PHOSPHATIDYLINOSITOL  
TRANSFER PROTEIN BETA  
ISOFORM

10    **Putative function**      phosopholipid transporter involved in lipid metabolism

**Confirmation by RNAi**      Slight reduction of G1 and increase in G2/M peaks  
indicating arrest in G2/M

15

**Line ID** 418/32  
**Category** Meiotic defects in testis: cytokinesis defects. Dark bands in eyes, dominant.  
**Reversion** ?  
5 **Map Position** 69C

**Rescue ID** G2E

**Rescue Sequence**

10 AGCTAAATAACAAACTCATTACTAGTATATTACTGCCGCCGATTTGCAAGCGC  
GTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGTTGTACGTCATCACTT  
AAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATTGATATTCCGCCCGCT  
GTGTGTGCGTGTGTATTTGCAAAAGAGTGTGTGTGTGTATGTGCATATGACTC  
GTGCGTTTAGCCGACAATTGGAGAAAAAGCATTAGAATCCCAATTGGCTAACT  
15 TGGCAGCGAAACAAAAACACCAAAGTGTTATTGGCAGATATATATGTTAATTA  
AATATNAAAAAGTGCGTGCGAA

**Genomic hit, Accession No.** AC006589

20 **Drosophila EST** SD01527 (AI530804), GH18602 (AI387906)

Rest of results same as line 1104/16

**Example 4 (Category 1)**

**Line ID** 1285/1  
**Category** Meiotic defects in testis: cytokinesis defects  
**Reversion** ?  
**Map Position** 85D1-5

**Rescue ID** D8E

**Rescue Sequence**

10 GTTCGCAAAAAATATATCTCACCGTGAGTGCGAAAGAGAAAAAGAGAAGCGG  
 AGAGGTGGAGAGCAAGTGGACATGAATCGTCGAGAGTCAGAGAGAGAGAGG  
 TGGAGAGGGTGAGCAGCTGTTGTCTGACAATAACATAATCAGCAACAATTTAT  
 GCTGTTTAAAAAGAGCAAGAGAAACGCTAATGAAGGGGAACACGGGCAGGGT  
 CAGGGGTTGGTGGATCCCCTACATATCTCTCTTTTACCGCCCCCGCTCTGGC  
 15 ACCCTCTCTGTCTGCTCTCCATTAGCCGCACACGTGCAAGCTTAGCATTCTATC  
 TGTCTGTCTCTGTTTGTGTTTGTGTTGCTAAGCCGAATTCT

**Genomic hit, Accession No.** CSC:AC014256

**Associated ORF**

Genscan ORF1 predicted sequences

>/tmp/aaaaakfaa|GENSCAN\_predicted\_peptide\_1|702\_aa

MIQRCVLLWIVCFCDLFLGLLFLKRKRNAHTPPPPQFTTYRHLLCYCFRNGEIM  
 ANICLSRLSVLEIVLLLRVPCAFYFVDYVPCLLSVLSEFLYHDQLKVFNRTK  
 25 QQHQQQQQQQQQQLYQQHQQQQQHYGPPPPYFQQLHQHQHQQQQQQQQQQ  
 HQQHMKFLGGNDRNGRGGVGVGTDAIVGSRGGVSQDAADAAGAAAAAAGV  
 YVFQQRPSGGVGVGVGGVGGVPGVGA VGSTLHEAAAAEYAAHFAQKQQQT  
 RWACGDDGHGIDNPDKWKYNPPMNANAAAPGGPPGNGSNGGPGAIGTIGMSG  
 LGGGGGGGAGGGNNGSGTNGGLHHQSMAAAAANMAAMQQAALAKHNHMI  
 30 SAAAAVAAQQQHQPQQHPQQQQQQQQAQNQGHPHLMGGGNLGNNG  
 LGIQHPGQQQQQQQQQQQQQHPGQYNANLLNHAAALGHMSSYAQSGGSMYDH  
 HGGAMHPGMNGGMPKQQLGPPGAGGPQDYVVMGGQTTVPMGAAMMPPQNQ  
 YMNSSAVAAANRNAAITTSTAKKLWEKSDGKGVSSSTPGGPLHPLQIPGIDPSS  
 VWKDHTWSTQGENILVPPPSRAYAHGGASDTSNSGNAGILSPRDSTCAKVVEYVF  
 35 SGSPTNKDSSLSGLEPHLRNLKFDDNDKSRDDKEKANSPFDTNGLKKDDQVTNSN  
 GVVNGIDDDKGFK

>/tmp/aaaaakfaa|GENSCAN\_predicted\_CDS\_1|2109\_bp

atgattcagcgcgtgcgtgttctctatggatagctctgcttctgcgactgttcttggggctcctgttccctcaaacgtaaacgcaacgca  
 40 cacactcccccccccccgcaattcaccacttatcgcatctacttctgtattgtttcgaatggggaaatcatggctaatttgc  
 cttagtcgtctttcagtttagaagaattgtttgttttacgcgtgccttgcgttttattttgttgattattattatgtccctgtctgtgt  
 ctgtgttatcggaatttttttaccatgaccagctcaaatgttttaatgcacaaaacagcaacaccaacagcagcagcagcagca  
 gcagcagcaactctatcagcaacatcaacagcagcagcagcaacattacgggtccaccaccgccctactttcaacagctacacca  
 gcaacaccaacagcagcagcagcaacaacagcagcagcagcaacaccagcaacacatgaagttttgggtggtaacgatgatcga  
 45 atggccgcggaggcgtcgcggttgccacggatgccatttaggatctcgagggtggcgtctctcaggatgccgccgatgcagctg  
 gtgcgccgcagccgccgcgtcggtatgtctccagcagcgtccatcgctgggtgggtggcgtcgccgtggcgaggagtg

ggtggcgggtgtgccaggggtcggagccgtaggctcgacctgcacgaggccgccgccgagtagccgccactttgcc  
 agaagcaacagcagacccgatgggcgtcggcgacgacggccatgggatcgataacccggacaaatggaagtacaatccgc  
 cgatgaatccggccaatgccgctcctggcgggtccaccgggaaatggcagtaatggtgggccggcgccattggaaccattggc  
 atgggcagcggattgggtggtggtggcgggcgggagctggcgggcgaaataatggcggtctgtgtacgaatggcggtctgc  
 5 atcatcaatcgatggccgctgcagctgcgaatatggcagccatgcaacaggcgggcggttgccaagcacatcacatgatat  
 cacaggcagcagccgagttgcagctcagcaacaacatcagcatccacaccagcagcatcccagcagcagcagcaacagca  
 gcaggcgagaaccaggggcatccacatcaccttatggcggtggcaatggactgggcaacggcaatggattgggcatacaa  
 catcccgccagcaacagcagcagcagcagcaacaacagcagcagcaacatcccggccagtacaacgcgaatctgttaacc  
 atcggtgctgccttgggtcacatgtcatcttatgcccaatcggtggcagcatgtacgaccatcatggtggagccatgcacccggg  
 10 aatgaacggcgcatgcccagcaacagccattgggtccaccggagccggaggacccagactatgtctacatgggtggc  
 cagaccactgtgccatgggagccgaatgatgccgccacagaatcaatatgaacagctctgtgtgtgcagctgccaatcgga  
 atgcagcgattaccacatccactgccaagaaattgtgggagaaatccgatggcaaggcggtatcctcgagcactccgggtggac  
 cgttgcatccctgcagatccccggcatcggggatccctcctcgtgtggaaggatcacacctggtccacacagggcgagaatat  
 attggtgccgccccctcgcgagcctacgcccattggaggcgctccgatactcaaacagcggaatgcgggcatactgagtc  
 15 ccgcgattcgacttgcgccaagtgttgatgtttcagtggctcgcccaccaacaagatagctcgtttccggattggaacc  
 gcatttgcggaatctaaggttgacgacaacgataagtcacgcgacgataaggagaaagcaaactctccgtttgacacaaacggtt  
 tgaagaaagacgatcaggtcacaaactcaaattggtgtgtcaacggcattgacgatgacaagggcttcaagtga

**Drosophila Gene Hit** TBLASTN of ORF1: pumilio protein (L07943)  
 20 **Human Homologue** TBLASTX with pumilio: Soares fetal heart NbHH19W Homo  
 sapiens cDNA clone (W77820)

**Annotated Drosophila genome genomic segment** AE003681  
**Annotated Drosophila genome Complete gene candidate** CG9755 – pumilio RNA

25 **Human homologue of Complete gene candidate** 1e-154 1944416  
 dbj|BAA19665| (D87078)  
 similar to D.melanogaster  
 pumilio protein (S22026)

30 **Putative function** Putative RNA binding protein which is localised to the cytoplasm.  
 Wild-type allele of pum involved in development of the abdomen  
 (embryos) and of the imaginal discs (larvae or pupae), perhaps  
 35 having a function in signal transport.

**Confirmation by RNAi** Only wild type profiles observed

**Example 5 (Category 1)**

5	<b>Line ID</b> <b>Category</b> <b>Reversion</b> <b>Map Position</b>	1389/1 Meiotic defects in testis:segregation defect, cytokinesis defect (Ck-09/32) NR 93B4-8
10	<b>Rescue ID</b> <b>Rescue Sequence 1</b>	2C9P GTTCTGGGGTGTGTGCGTGCTTGCGAGTGTGCCTGTGTGTGTGTAGGAAAGGAG CAAGAAGCAGCAGCAGCGGCAGCAGTAGAAATAGCAAAAGGAGGCAGCAAC AACATAAGCTAGAGAAACCGCCAGCAGCAGCCCCCTAATAAAGAGCAGAGA AAAAAATGAGTTCAAGTTGTGAAAGGTGTGTGCCGTTACACTACAACTACAA 15 CACCACCATCAGCGGCAGCAAAGAAATACAACAACAAATACGGCAATCTCCA GACAACGCGAATGTTCGAAATTGTGTATACAATTTATTAAGAAAGCAAGAGCA GCAACAACAATGACCAGCTGCAGTTCATCAGCGGTGTCCTCCTGAATGCCGCT GTCGTCTGTTGGTGTCTGCCACCGGCGGTTCTCAATAATAAGGGCAGGAGGAG CTGCTTAGGTGCACACAATGTAGTTTGGCTTGGTGAATGCTTCTCTTTTTGTG 20 CTGCTGGCGCATACGTTCTCTCTCCCTCATGATCTCAGTTGTCTGCATCGA TGAGCCGCCACCAACGGTGGCTTCTTCTGCTCCTCTTTGGCAACGGACTGCTG CAGTCTTGCCAGAATTTTCTCTAAATACTGAGCTTCAACTTGGTCTGCTTGGT AATGGTATACCATAAGCCATGGACTTGATGCCCTACAAAGCTCTGTGATTG AAATGGGATGCA
25	<b>Rescue ID</b> <b>Rescue Sequence 2</b>	2C9E CCCCGAACGCACCTTTATATATATAAATATATATATTATTTTCTTTCACTTATTTT CGTTTCGGCCGCGACAGCGAATATGCAATTTTCTCTCAATTGATTTTTTTACA 30 CACTCGCACTCCTTTTACATGCGTGCAGTTTATGTTGCTATTGCTGCTACTGC TGCTGTTGTTGTTATTGTTGTTCTGGCTGCCGCTGCAGTGCAACTTGTAACACT TTCACATTTATGACATAATGCACTGGCCATATTTTGGCTTGGCTCTCCGTTTGT GCAACTGCATGTTCCCACTGCTTTTTTAATATTTATGCTGCAGTGCGTGCAAAT TCGAACGCGAGACGATCCGCTTTTCGCTGCATCTATGCGCTGAAGATGTGCTG 35 CAGTCGATGGGCTCGTCGATAGTGGGAAGGCTCGGTGCCGGCACTATCGATT CCAACACCATAACGATAATATCGGCTAAAGTTATCAATATCGAAGTTTACTATA TTTCGGGTTTTTACGTTTTAAATCTACCTTATCAACATTTTTGNAAGAAGTAAA AAGTAGTTCTCTTATGGATGCATC
40	<b>Drosophila EST</b>	several including LD10379 (AA816796)
45	<b>Annotated Drosophila genome genomic segment</b> <b>Annotated Drosophila genome Complete gene candidate</b>	AE003733 CG3421 - novel protein with weak homology to myosin

5	<b>Human homologue of Complete gene candidate</b>	Ensembl predicted Gene:ENSG00000071333 Clone:AC022505 Contig:AC022505.00011 5.60E-37 (predicted protein with Core domain in kinesin and myosin motors ENSG00000087179)
10	<b>Putative function</b>	Possible novel motor protein involved in cytoskeleton organization
	<b>Confirmation by RNAi</b>	Marked reduction of G1 and G2/M peaks indicating fewer cycling cells

### Example 6 (Category 1)

<b>Line ID</b>	293/9
<b>Category</b>	Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, very high polyploidy)
<b>Reversion</b>	NR
<b>Map Position</b>	66B

Rescue ID 2G5E

## 10 Rescue Sequence

GTACAAACGAATTATTTGTCTCCTTGTGCGTTCGTTTTATTGTGTTTCGAGTTCT  
GTTGGTGTGTGTTTTTGTGTATGTTCCACGAGTTGTTTCGCATTAAAAAATTAAC  
TGCAGAAGATCCATGGAAATGGAGACCATTGAAGAGCAATCGAAGTGCGGTG  
AGTACTGAAAGAGGGCGCGGGGCGTGGCAGCTCCAAATGGCCGGCGAATTTA  
15 TCATTTTTCAATGTCGTCCAAAGGGGTTGGGTACGGGGTAAAACCATTCGG  
GGCCAAAAGATCCTCATAAAAAATGTCGCTGCCAGCAAATGCAAAAAATAAA  
ATAAAATAAGAACGACTATAAGTACATCTTTGTGTGTATTTGTGTGACTAAAA  
AAGCAACGGCATCGTGTGCANATATTTTAATCTTTNTTCTGAATTTATTTTCG  
GTGTACAAAATATTTATCGCATAAATGCGAAATGCCTCCCTCTCTTCATCATCG  
20 T

**Genomic hit, Accession No. AC008303**

### Associated ORF

25 Genscan ORF1 predicted sequences >20:53:38|GENSCAN\_predicted\_peptide\_3|261\_aa  
MMDNDDALLNNGGPQSGAETVYGTEDNNMVMSEKCRIFPATQRTGFVGATFSG  
VLLLDL GALQHCDVIRIDVNIATLEQIKRERQEELAARERIRAQIAADRAEQAQRF  
NTPDISSTTNSVAATAASNVTDDASVSSVDETRLQIRLPGGIQRTKSF PAGEVLAT  
VRVYVRNEMLAASDVRDFTLATSYPREFQTEDEVKTLNELNLVPNAVVLVLT  
30 EOVPNADDOTAKRSASTKRTKTHRHKROLMADEPOSDHYKN

>20:53:38|GENSCAN predicted CDS 3|786 bp

atgatggacaacgatgatgcactgctcaacaatggaggaccacagtcggagctgaaactgtctacggtaccgaggacaacaac  
atggtcatgtcggagaagtgcgcgcatattccggcgactcagcgtactggatttggggcgagcgttttcgggagtgctgcttctt  
35 gatcttggtgccctccagcattgtgatgtgatccgattgatgttaacattgcaacgctggaacagattaagcgtgagcgtcaggag  
gagctggcggccaggaggcgcattcgtgccaaattgcagccgatcgggcagagcaggcacaacgttttaacgccggacat  
tagcagcacgaccaattcgggtggcggccaccgctgcctcaacgtgatcacaacagacgcctcggtgagttcgggtggacgaga  
cgaggctcgagatccgactaccggtggcattcagcgcaccaaatcctttccagccggcgagggtgctggctaccgttcgtgtcta  
cgtgcgaaacgagatgctggcggcgagcgtgtacgcgactttaccctggctaccagttaccacgaaggagggttccaaacgg  
40 aggacgaggtcaagacctgaacgagctaaatctagtgccaatgcggtggttctgtgtgtgaccaaggagcaagtgaatccag  
ctgatgaccagacagcaaacgatcagcaagcaccaaacgcacaaaaacacagacacaagcggcaattgatggcagacga  
gccacaatctgaccattataaaaactga

45 ***Drosophila* Gene Hit** rescue sequence: pebble (rho1 GTPase exchange factor)  
(AF136492)

**Human Homologue** BLASTX with pebble: KIAA0337 (AB002335)

***Drosophila* EST** SD09146 (AI542703), SD01796 (AI530981)

**Annotated *Drosophila* genome genomic segment** AE003557

5 **Annotated *Drosophila* genome Complete gene candidate** CG8114 - pbl pebble rho1  
GTPase exchange factor

10 **Human homologue of Complete gene candidate** 2224615 dbj|BAA20795|  
(AB002335) KIAA0337  
[Homo sapiens (3e-21 ) also  
mouse homologue 3e-95  
42359 transforming protein  
(ect2) - mouse >gi|293332  
(L11316) ect2 [Mus  
musculus]

15 **Putative function** A guanyl-nucleotide exchange factor involved in signal  
transduction which is localised to the mitotic anaphase. pbl is  
required for the formation of the contractile ring and the initiation  
of cytokinesis in *Drosophila*

20 **Confirmation by RNAi** Slightly reduced G1 and G2/M peaks indicating fewer  
cycling cells

<b>Line ID</b>	542/3
<b>Category</b>	Mitotic defects in brain: cytokinesis defect (very high polyploidy)

Reversion NR

5      **Map Position**                      66A

Rescue ID 2A1E

## Rescue Sequence

GTCCAGTTAATGAAAGTAAACGAATCGAGTACAAACGAATTATTTGTCTCCTT  
GTGCGTTCGTTTTATTGTGTTTCGAGTTCTGTTGGTGTGTGTTTTTGTGTATGTT  
10 CCACGAGTTGTTTCGCATTAAAAAATTAAGTGCAGAAGATCCATGGAAATGGA  
GACCATTGAAGAGCAATCGAAGTGCGGTGAGTACTGAAAGAGGGCGCGGGGC  
GTGGCAGCTCCAAATGGCCGGCGAATTTATCATTTTTTCAATGTCGCCCAAAGG  
GGTTGGGTACGGGGTAAAACCAATTCGGGGCCAAAAGATCCTCATAAAAAA  
TGTCGCTGCCAGCAAATGCAAAAAATAAAATGAAATAAGAACGACTATAAGT  
15 ACATCTTAGTGTGTATTTGTGTGACTAAAAAAGCAACGGCATCGTGTGCGCANA  
TATTTTAATCTTTTTTTCTGAATTTATTTTCGGNGTANAAAATATTTATCGCATA  
AATGCGAAATGCCTCCCTCTCTTCATCATCGNTTCCCCTNACTCTCCCTCTCTT  
CGCCCGACACTGTACCGACGCAAGAAGAAC

20 **Genomic hit, Accession No.** CSC:AC018042  
***Drosophila* EST** SD09146 ( AI542703), SD01796 (AI530981)

rest of results same as line 293/9

**Example 7 (Category 1)**

5	<b>Line ID</b> <b>Category</b>	229/30 Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects (Mitotic higher level of condensation, polyploidy, Meiotic: Ck05/07)
	<b>Reversion</b>	?
	<b>Map Position</b>	91F
10	<b>Rescue ID</b>	A7E
	<b>Rescue Sequence</b>	TCTTGGCCAAACAACGCGAGCAGCTGATGTCGCATGGTGGGAAAATGAGGGT GGCGCGAGTGGAAGTTGCCATATCGCTGCGATCACAAGCAGCAAATATGGAA 15 GATTAAGCGGAAAACGAAAGACAAAATAATTACAATCAAACAACCGAATTAT AAAAAGAAAATGGTTTGTCTCCGAGTTCGTTTAAATATGCTTATCTACGTATC AATTAAAAAAACCGTAGAAAGAAATTCACGATTCACCCTAATCTAGCTAAGA CACCAACCAAAAATTTCCGATTTACTTTCAGTTGAAGTTGTTGTTACACACTTT TCTTGTCGATGTTTTGAAGCGCCCATTTGAAATTGATCATTTGAATGTTTTTCCA 20 AATTACCCACATCCATTACAATAAATTTAAATTGCTTATTATTTGATTTTACT TGGGAAAATCCCGTTGCCAAATTGGAATTACAATTCCAGCTTGGAATCCGTCA AACTTTACAACATAAACTTATTGTTCTTTTCCGGACAATGCTTCCA
25	<b>Annotated <i>Drosophila</i> genome genomic segment</b> <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	AE003686 CG6284 - novel protein possible sir2 family of transcriptional regulators/telomeric silencing
30	<b>Human homologue of Complete gene candidate</b>	gi7706710 0268A424791DE5BF  ref NP_057623.1  sir2-related protein type 6 [Homo sapiens] (1.10E-74)
35	<b>Putative function</b>	Putative transcriptional regulator
40	<b>Confirmation by RNAi</b>	Complete loss of G1 and G2/M peaks indicating fewer cycling cells

**Line ID** 1104/16  
**Category** Mitotic defects in brain, Cytokinesis defect (no overcondensation of diploids, high polyploidy)

**Reversion** R

5 **Map Position** 92A

**Rescue ID** B5E

**Rescue Sequence**

10 GTCCGGAGCGGAGCTAAAGTTCGATGTTCGTGCAAAACACTTCGATTCCGATA  
 GGCGGATGCTATCGATTTTCGGCGATGCCCCGTTGGTCACACTTGGTGGTGGGCG  
 CTGCCCCGTCGCCGACTATCGATAGCACAAAGCGGGTTATTTAGGTGTGCGCAGC  
 TTGTAAGGGTGACTCATGCTGTAAATTAATAAAAAAGTTAATGAATATAA  
 TATAGTTATAATAAAATTATATATAAATCTATAAGATCAAAGATCATCAGTTA  
 TCATTTATCATTTGATTATATGAAAAACAAGAACAGAAACAAGATTTAATAGG  
 15 TTTTGTAAATGTGAAAATGTGGGTACCCCCAATTCTTATTCGAAATTAAATAA  
 CCTAAAGAACAGTTATACACAGATAGGTAATTTGCACATAAGCCAAATTTTGT  
 CTAGAATTCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCCGTGATACGCC  
 TATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTA

20 **Rescue ID** B5P

**Rescue Sequence**

CTCCGGACACGCAGTAGCTAAATAACAACTCATTACTAGTATATTACTGCCG  
 CCGATTTGCAAGCGCGTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGT  
 TGTACGTCATCACTTAAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATT  
 25 GATATTCCGCCCGCTGTGTGTGCGTGTGTATTTGCAAGAGAGTGTGTGTGTGT  
 GTGTGCATATGACTCGTGCGTTTAGCCGACAATTGGAGAAAAAGCATTACCAA  
 TCCCAATTGGCTAACTAACTAAAGTTGGCTTGGCCAAACATAAACAAAAAGT  
 GCGGGCGCAGCGATTTGGCAGCGAAACATATACACCAAAGCGCTATTGGCAG  
 ATATATATGTAGATTAAATATAGAAAGTGCGTGCGAAGGTTAAGAGTCGAGT  
 30 GCAAGTGCATTTATATTTGGAAATAATAAATGCTACAAT

other results same as 229/30

**Example 8 (Category 1)**

**Line ID** 343/5  
**Category** Mitotic defects in brain: cytokinesis defect  
(very high polyploidy, chromosomes entangled?)  
**Reversion** NR  
**Map Position** 75B

**Rescue ID** C6E

**Rescue Sequence**

GGTTTCGAGTTCGTTTCGGTTTCGGCCTCTCCGTTTCGGCTCTCTCTCGCCATCCC  
GCTGCCGCACACATTGGCCTCTCTCTCGCAGCTCCACATTCGAAGGTGGCTGA  
CCGAAATGTGGGTCACGACAATGGCGGGGTTTCGTTGAACTGAACCACCGCCG  
CAGTCGCTGCCGTGCTCGCTGCTCTGCCCTCTGCTGACGTCGTTAACGTTTTGGG  
GCTTTCGGTTACGTAGCTCGTGTGCGAGCGAGAGGGGCTACTAGAGGGACTGC  
GACACACAAGTTGTGTGCATTTTTTGGCCCCAAAAAATCACAATGGGCACAAA  
ATATTATTTAATACATCACATAATTGTTTAATCATCTGGCTGGAAAGTGTCGAG  
TTCATCGAACTGCCAGCGATTGACAAATTGCGATTTTCAATGCGGCAAAAATA  
TTTACTCAAGCAAATTGTTTGCACCTTCGTTAATTAGGCGGGGAGTGCCGCCAA  
ATTGGGTCATATTGCAGAAAGTATCCAAGAAAGTTGGAGAAACAAGCTGCTTAA  
ACATTAATTAACACACACCTAAATGGATACATTTGCTACAAACAATTATAAAT  
GTTACCCTTATATTAATTTTCAAATTTCTAAATAATCAA

**Genomic hit, Accession No.** CSC:AC015427

**Associated ORF**

Genscan ORF1 predicted sequences

MVCAMQEVAADVQHQQQQQQQLQLPQQQQQQQQTTQQQHATTIVLLTGNGGGNL  
HIVATPQQHQPMHQLHHQHQQHQQHQQQAQKSQQLKQQHSALVKLLESAPIKQQ  
QQTPKQIVYLQQQQQQPQRKRLKNEAAIVQQQQQTPATLVKTTTTSNSNSNNTQT  
TNSISQQQQQHQIVLQHQQPAAAATPKPCADLSAKNDSSESGIDEDSPNSDEDCPN  
ANPAGTSLEDSSYEYQCPWKKIRYARELKQRELEQQQTGGGNAQQQVEAKPA  
AIPTSNIKQLHCDSPFSAQTHKEIANLLRQQSQQQQVVATQQQQQQQQQHQQHQQ  
QRRDSSDSNCSLMSNSNSSAGNCCTCNAGDDQQLEEMDEAHDSGCDDDELCEQH  
HQRLDSSQLNYLCQKFDEKLDLTALSNSSANTGRNTPAVTANEDADGFFRRSIQKQ  
IQYRPCTKNQQCSILRINRNRQCQYCRLLKCIIVGMSRDVLRLEQPKAGAKNKSCE  
PSKNSTVNQINSKLELGNSNEMK

>21:55:09|GENSCAN\_predicted\_CDS\_1|1533\_bp

atggtttgtgcaatgcaagaggttgctgccgtgcagcatcagcagcagcaacagcaactccagttgccccagcagcaacagcag  
cagcagcagacaacacagcagcaacatgcaacaactatagtgtgctgacgggcaatggcggcggtaatctgcacattgtgcc  
acaccgcaacagcatcagccgatgcatcagctccaccatcagcatcagcatcagcaccagcagcaggccaagagcc  
aacagctgaagcaacaacactcggcgtggtcaagttgctggagtcggcgcccatcaagcagcaacagcagacgccaagca  
aattgtttacctgcagcagcagcagcagcaaccgcaacgcaaaaagactgaaaaacgaagcagcaatcgtacaacagcaacaac  
aaacacctgcaacactagtaaagacaacaaccaccagcaacagcaacagcaacaacacccagacaacaatagtattagtcag  
cagcaacagcagcatcagattgtgtgagcaccagcagccagcggcgagcaacaccaaagccatgtgccgatctgagcg

ccaaaaatgacagcagagtcgggcatcgacgaggactccccaacagcgatgaggattgccccaatgccaaacccggcggggcac  
 atcgetcaggacagcagctacgagcagtatcagtgccctggaagaagatacgtatgcgctgagctcaagcagcgcgagtg  
 tggagcagcagcagaccaccggaggcagcaacgcgcagcagcaagtcgaggcgaagccagctgcaataccaccagcaac  
 atcaagcagctgcactgtgatagtccttttcggcgagaccacaaggaaatcgccaatctcctgcgccaacagtcccagcaac  
 5 aacaggttggtggccacgcagcagcagcagcaacagcagcagcagcaccagcaccagcaacaacgaaggatagctccgaca  
 gcaactgctcgtgatgagcaactcgagcaactccagtgcgggcaattgtgcacctgcaacgctggcgacgaccagcagctgg  
 aggagatggacgaggcccacgattcgggctgcgacgatgaactttgcgagcagcatcaccagcgactggactcctcccaactg  
 aattacctgtgccagaagttcgtatgagaaactggacacggcgctgagcaacagcagcgccaacacggggagggaacacgccag  
 10 ctgtaacagctaacgaagatgccgatggattcttcgccgctccatccagcaaaagatccagtatcgccgctgcaccaagaatca  
 gcagtgcagcattctgcgcatcaatcgcaatcgttgcaatattgccgcctgaaaaagtgcattgccgtgggcatgagtcgcgatgt  
 tctgcgcctagagcaacctaaagctggtgccaaaaataagtcattgtgaaccgagcaaaaattcgaccgtcaaccaataaacagc  
 aaactcgaactcggcaacagcaatgaaatgaaatga

***Drosophila* Gene Hit** TBLASTN with ORF1: ecdysone-inducible gene E75B (X51549)  
 15 and nuclear receptor superfamily protein (U01087) BLASTN with  
 genomic sequence matches ecdysone inducible gene

**Annotated *Drosophila* genome genomic segment** AE003522

20 **Annotated *Drosophila* genome Complete gene candidate** CG8127 Eip75B ecdysone-  
 inducible gene E75B nuclear  
 receptor NR1D3

25 **Human homologue of Complete gene candidate** ORPHAN NUCLEAR  
 RECEPTOR NR1D1 (V-  
 ERBA RELATED PROTEIN  
 EAR-1) (REV-ERBA-  
 ALPHA) Q15304 ( 9.40E-74)

30 **Putative function** Ligand-dependent nuclear receptor, putative transcription factor

35 **Confirmation by RNAi** Slightly reduced G1 and G2/M indicating fewer cycling  
 cells

**Line ID** 448/23  
**Category** Mitotic defects in brain: cytokinesis defect  
(very high polyploidy)  
**Reversion** NR  
5 **Map Position** 75B

**Rescue ID** 2G4E

**Rescue Sequence**

10 GCTGGTGGACGCTGCTTTCATTCGCAAATTGCTCGTCGTTGGCAGCGGTTGTGC  
AGAGCAAGAAAAGCGCGCGGAAAAACCAAGCAAAAAATTAATACAGCTGGAT  
CAAGCGAAAGAGATAGAGAGCAGAGTCAACAGCAACAAATGTTCAATAGCA  
AATGATATCGCATATTTTTGTTGGTGCCAGTGAAGTGAGATCAAAGTGAAGTG  
TGCAATGTTCTTATTAGCAAATCGTAGAGCAACCAACAATCGAGAGTTCAAG  
15 TGCAAGAGGTTGCTGCTGTGCAGCATCAGCAGCAGCAACAGCAACTCCAGTT  
GCCCCAGCAGCAACAGCAGCAGCAGCAGACAACACAGCAGCAACATGCAAC  
AACGATAGTGCTGCTGACGGGCAATGGCGGCGGTAATCTGCACATTGTCGCCA  
CACCGCAACAGCATCAGCCGATGCATCAGCTCCACCATCAGCATCAGCATCAG  
20 CATCAGCACCAGCAGCAGGCCAAGAGCCAACAGCTGAAGCAACAACACTCGG  
CGCTGGTCAAGTTGCTGGAGTCGGCGCCCATCAAGCAGCAACAGCAGACGCC  
CAAGCAAATTGGTTACCTGCAGCAGCAGCAGCAGCAACCGCAACGCAAAAGA  
CTGAAAAACGAAGCACAATCGTACAACAGCAACAACAACACCTGCAACAC

**Genomic hit, Accession No.** CSC:AC015427  
25 **Drosophila EST** GM03519 (A801874)

Other results same as line 343/5

**Example 9 (Category 1)**

5	<b>Line ID</b> <b>Category</b> <b>Reversion</b> <b>Map Position</b>	36/1 Meiotic defects in testis: cytokinesis defects (Ck-04/06) ` R 79C
10	<b>Rescue ID</b> <b>Rescue Sequence</b>	A8B GAGTAAAGTAAACTACAGAGAAAAAACGCTTTACGGCGAGAGAACGCTTTAA TTATACTTAATTTGTTGTTAATCAAACGCACAGAGCACACAACACAGAAACAC AAAACACCGCTTGGGAAAAATCTGTAGGTAGANGAAAGGAGCTCACGTTTTT CTGGTGCAGATCGAAATCGGTATCGGGTTTATTTCGCTTTGCCGGATTGTTACTT 15 CACGTTTGTTAATTGCGTTTCTTTGTTTCTTATTCTCCTGCGCACACTTTGATTT GCGTTTGCAACTCGCAATTGCAATTGGCATTGCTATGCGACAACGCGGTT ATTTCCGGTCCGTTTACTTTTCCAATGGCTTGCCTACACACCGCCAAACTTTGG CTTGAACCTGGGATATTGTTTGCCCGAATTCCTGANAAATTTTTCCTT
20	<b>Genomic hit, Accession No.</b>	CSC:AC013886
25	<b>Associated ORF</b> Genscan partial ORF1: >18:33:59 GENSCAN_predicted_peptide_1 99_aa CICFALLGLLIRRKLMVVFGSTSRKAQSLESRRRAKNTSQKIGNQYPKFSQVCGKPS KSNDNRNNGSCRANANCELRVANANQSVRRRIRNKETQLTNVK  >18:33:59 GENSCAN_predicted_CDS_1 300_bp tgtatctgcttcgccctgcttgggtactcattcggcgaaaattaatgggtggtggttcggttctacgtcgcgcaaggcacagtctctaga gtctcgcagagctaagaatacatctcagaaaatcggaaccaatatcccaagttcagccaagtttgcggcaagccatcgaaaagt 30 aacgaccgaaataacggcagttgtcgcatagcaaatgccaattgcgaattgcgagttgcaaacgcaaatcaaagtgtgcgcagg agaataagaaacaaagaaacgcaattaacaaacgtgaagtaa	
35	<b>Drosophila Gene Hit</b> <b>Human Homologue</b> <b>Drosophila EST</b>	rescue sequence and TBLASTN with ORF1: nucleic acid binding protein (mub) (X99340) BLASTX with nucleic acid binding protein: poly(rC)-binding protein 2 (hnRNP-E1) (S42471) several including LD32520 (AA951799 BLASTN matches nucleic acid binding protein (X99340)
40	<b>Annotated Drosophila genome genomic segment</b> <b>Annotated Drosophila genome Complete gene candidate</b>	AE003596 CG7437 - mub mushroom bodies RNA binding protein
45	<b>Human homologue of Complete gene candidate</b>	4826886 ref NP_005007.1 pPCBP2  poly(rC)-binding protein 2

>gi|542853|pir||S42471 (4e-75)

5    **Putative function**    A putative RNA-binding protein specifically expressed in the CNS of *Drosophila melanogaster*

10    **Confirmation by RNAi**    Only wild type profiles observed

**Line ID** 472/22  
**Category** Female sterile  
 (anaphase bridges, lagging chromosomes)  
**Reversion** ?  
 5 **Map Position** nd  
**Rescue ID** sau 5'spl

**Rescue Sequence**

10 GCACGATCNCTAAAGTCTNGCANAGCTAAAAATACATCTNAGAAAATCGGCA  
 ACCAATATCCCAAGTTCAGCCAAGTTTGCGGTGTGTAGGCAAGCCATCGAAAA  
 GTAACGACCGAAATAACGGCAGTTGTGCGCATAGCAAATGCCAATTGCGAATT  
 GCGAGTTGCAAACGCAAATCAAAGTGTGCGCAGGAGAATAAGAAACAAAGA  
 AACGCAATTAACAAACGTGAAGTAACAATCCGGCAAAGCGAATAAACCCGAT  
 15 ACCGATTTTCGATCGGTGCGGGCCTCTTCGNTATTACGCCAGNTGGCGAAAGGG  
 GGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACG  
 ACGTTGTAAACGACGGCC  
 ANTGCCAAGCTCTGCTGCTCTAAACGACGCATTTTCGTACTCCAAAGTACGAAT  
 TTTTCCCTCAAGCTCTTATTTTCATTAAACAATGAACAGGACCTAACGCCNGT  
 20 AAC

**Rescue ID** Sau 5'splac

**Rescue sequence**

25 GTTGTGATCNTCTTGGTNAATCNNNTTGGAAATTCCCCTAANGCTTCCGACAA  
 TGACCCNGNCNTACNNAGCAAANAATNGNAGNACNNGCNGNTGGNCGTANT  
 ANCAANAACAGGCCCGCACCAGATCGAAATNNGGNATCGGNTTTATTTCGCTTTGC  
 CGGATTGTTACTTCACGTTNGTTAATTGCGTTTCTTTGTTTCTTATTCTCCTGCG  
 CACACTTTGATTGCGTTTGCAACTCGCAATTCGCAATTGGCATTGCTATGCGA  
 30 CAACTGCCGTTATTTTCGGTCGTTACTTTTCGATGGCTTGCCTACACACCGCAA  
 CTTGGCTGAACTTGGGATATTGGTTGCCGATTTTCTGAGATGTATTCTTAGCTC  
 TGCGAGACTCTAGAGACTGTGC

Other results same as line 36/1

35

**Example 10 (Category 1)**

<b>Line ID</b> <b>Category</b>	459/2 Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects: (mitotic: high polyploidy, no diploids, higher mitotic index, meiotic: Ck-01/05)
<b>Reversion</b> <b>Map Position</b>	NR 66B1-6
<b>Rescue ID</b> <b>Rescue Sequence</b>	2D5P GCTCCGTTTCGAAAGTTGAGAGAGACTTGAAACATATGTTTCGGCGTTGCTAGAG CTGGTCGGCTACCGATAGAAACATCGATAGGTCCGATGTTTTTTACTCGTATAT TGATTCANAGTTTGGCTATCGATGTTTTTAGAGTGCCCGCACATTATCTATTTT CATCTCTATTTTCGTTGGTATTTTTTGTATTTTATGACATTTTCGACTGCAAAAGC AGGATGGCAACGCCAGATTGCCGCGAAAGTACGTTATTTTTAAATTGGCGCAT TGAATATGAAAAATTGCAGGCACATACAGTTTCTAATAAATAATAGCAATAAT TATTATTTAGCTTGTATCATACGAAGTGCACATTACAGCTACGCATCTGAAAT AATAATTTTAATATATCGTCTTTTCTCCCATCGATAGAGTTCCGCGCCTATCGA TATATCGTTGATCACCAAATAAATAAACTAAATAACGCCGCAATGGAACAC GCGACGAGTGAATTGAGGGAATTTATCTCAGATCTTGTAATTCCGCACCCACGT TGCAATGGTAACATCAATCCGGATCACATCACAATGCTGGAAGGCACCCAGA TCCAGAACAG
<b>Annotated <i>Drosophila</i> genome genomic segment</b> <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	AE003557 CG8038 - novel gene ribonuclease P homology CG7892 nmo - protein serine/threonine kinase involved in eye morphogenesis
<b>Human homologue of Complete gene candidate</b>	CG8038- 5e-24 4309676 gb AAD00893  (AF001176) ribonuclease P protein subunit p29 [Homo sapiens]  CG7892- protein kinase mitogen-activated 7 (MAP kinase)' gi:4506093 and gi7706445 D919050533B3C33A [ref]NP_057315.1  nemo-like

kinase [Homo sapiens]  
(3.30E-174)

- 5    **Putative function**    CG8038: tRNA processing enzyme Ribonuclease P protein subunit  
CG7892: a protein serine/threonine kinase involved in cell cycle,  
possibly targeted to cytoskeleton
- 10   **Confirmation by RNAi** Both showed a marked increase in G1 peak indicating arrest in  
G1

**Example 11 (Category 1)**

	<b>Line ID</b>	623/8
5	<b>Category</b>	Meiotic defects in testis: cytokinesis defects
	<b>Reversion</b>	?
	<b>Map Position</b>	37E1-3
	<b>Rescue ID</b>	2E2E
10	<b>Rescue Sequence</b>	CTACGGGCATTTCGCATGTTTCGAACATCTGGTGTAAACAAGTTCTGAGCAGTGT TGCCAACTCTTCAGTTAAACAGTTAAAAATAGCTAAAAAATGTTGACGGTAGC TAAATTATAAAGCTAGAAAAGAAATGATATATGATAAAATAAGTATTTTCGACT CACAGCATTTATTATTTAAGACGGTCAGATGAAGTTACAAAAATCCTAAATTG 15 GCCCGCTGTATCTAAGAATTAATACCAAGAAGTTGTCATCAAAGGTCGAACTC GACGGAAATTCTACTTTGAGTTTTTAAATTTAATAAATATGTATTTAAAATTAT GTAAATTTGTTTGTAACAAAAATAGTATATAGTATAGTAATAGTAGTTAAG TAGTTTTAAAAATGGCCAGATCAAAGACTTTTGAGATATGATACTAATCAAAA GTCGAATTCGCGGAATTAATTCTTGAAGACGAAAGGCCTCGTGATCGCCTATT 20 TTTATAGGTAATGTCATGATAATAATGGTTTCTTAGACGCAGGTGGACTTTTCG GGGAAATGTGCGCGGAACCCCTATTTGTTATTTTCTAAATACATTCAAATATGT ATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGG AAGAGTATGAGTATTCAACATTTCCGGGCGCCTTATTCCTTTTTTGGGCGGCAT TTGCCTTCCTGTTTTTGTACCCAGAACGCTGGTGAAAGAAAAGATCTGAAGA 25 CAGT
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003662
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG17559 dnt - doughnut protein tyrosine kinase
30	<b>Human homologue of Complete gene candidate</b>	Homo sapiens RYKreceptor tyrosine kinase GDB:21773
	<b>Putative function</b>	growth factor transmembrane receptor protein tyrosine kinase involved in cell growth and maintenance
35	<b>Confirmation by RNAi</b>	Only wild type profiles observed

**Example 12 (Category 1)**

**Line ID** 629/14  
**Category** Meiotic defects in testis: cytokinesis defects  
 5 (Ck-06/09)  
**Reversion** NR  
**Map Position** 64D  
  
**Rescue ID** 2A9X  
 10 **Rescue Sequence 1**  
 GACGGGAGGAAGTAAGTGGGAGGAGAGAGTAGTGCCTCTTTTTTTACTGGAGA  
 AATGGACAAACTCTGGGAACTGCGAACTGCGAACTAACCGAGGCAAAAATTG  
 AGAAGCGAGCTGAAAGCGGAATTCAAACAACGCAGCGCTGACGGCGACGCCG  
 GCAGAAGCAGCGCCGCACAAGGCATGCGCACAGAGAGTAAGAAAGAGCGCG  
 15 GCTAATGAATGAATGAACGAGGCGGAATGCGGGAAGAGCGCAGAGAGGCGC  
 AATGACAAAATAGTTGTAGAAAAGCGCCGGCAAGCGGAACTCCACACTCTTT  
 CTCACTCTCTCTTTCCACCCACACCCCTAGTTCACCGGAAAAAGAAAATTCGTT  
 TGCGGCGGGGGTGTATTTTTCACCAAAAAGAGAGTGTGTGCAAAACGCTAGA  
 GAGAGAGAGAGAGAGAGAAAGAACTGACGTCAGTTCTGCCTCCGTCGACGCC  
 20 GCTGCCGCGCTCCCAAAGCGCCACCACCCAAAAAACGCGAGAAGAAGCAGA  
 ACAAACACACACAAAAATTCGCACAGTGGAGCAGAAATCAAGC

**Rescue ID** 2A9E  
**Rescue Sequence 2**  
 25 CTCCCGTCGTTTTGAGATCAGCTGCTCTCGCAACAACAACAACATAACTGTA  
 GTTACCGTCTCTTTTGCATCGTTTCGTTTTTCGTTTGTGTGCGCCAAGTGATTGTGT  
 GTGTGCGTAAGCTTAAAGCTGACTAACAACGAAACAAGAAAAAATATAAA  
 TTATAGGAAAATTGTTAAATTATAACCAGAAAGAGAGCGGCACCTTACGTGTGT  
 TATTGTGTGCGTGTGCTTTAAAAAGATATAAAAAATAGCAATAGAAAGTTATTA  
 30 AAGCGTTGGCAAAAAAGTCCAACGAACAGCGAGAGGAAGCGGAGAACGAAA  
 TAGTTAAAGCCAAAGTCGCTGCCGACGTGCGCACTTGAAAACGTGCAAAAAGTT  
 GTTAAACACACCAGTGTGTGTTTCGTGTGTGTTTTTGCCGGCGTGCCAGTGTGCG  
 TGCGCCTAGAAAAGAGTAAAGAAGCAGAAGAAAAGGAAGAAGCCGAAGAAG  
 CAGCAAAAGAAGCCGACAGCAAAAAGTAAATAAAATCAAATGCCCCCTGGCA  
 35 GAATAATATTAAATTAAGACACATACTCAAATTAATAAC

**Genomic hit, Accession No.** CSC:AC015076

40 **Drosophila EST** LP08767 (AI295205)  
**Annotated Drosophila genome genomic segment** AE003567  
**Annotated Drosophila genome Complete gene candidate** CG10668 - novel with  
 homology to ssDNA/RNA  
 binding proteins  
 45 **Human homologue of Complete gene candidate** CG10668 - 3e-12 4506449

ref[NP\_002889.1|pRBMS2|  
RNA binding motif, single  
stranded interacting protein 2  
>gi|1082

5

**Putative function**      Possible single stranded DNA/RNA binding protein

10    **Confirmation by RNAi**      Slightly increased G1 and reduced G2/M indicating G1  
arrest

**Example 13 (Category 1)**

**Line ID** 653/12  
**Category** Meiotic defects in testis: segregation defects, cytokinesis defect  
 5 (Ck-07/35)  
**Reversion** NR  
**Map Position** 75B

**Rescue ID** I5E

10 **Rescue Sequence**  
 GTAAAAGCTTAGCCCATGGCGTCGACGTCGACTGCGACAGCGACGCTAGCCG  
 AGGCAGTGACTGCGACGTTGGCCACTTTTCGCCTTCGTTTCGCTGTCGTTTCA  
 GTTGTCTCTCGTTGCTCAAAGCGCGCGGCACGCGAACGCTCTGAAATCCCAAG  
 TTACAACAGCAACATCAAGCAGCAGCAACAACAGTGATTCGCTGGCAAACAA  
 15 ACAAACAAACCAACATATTTTTGTGTATCAATTGTCGGCCTAAACTTCACAT  
 AAAAGTGCGTTCAATACGAAACAAATATATTTGTATATATAGAGAGCGAAGC  
 AATCGGTTGCATAAATTGAATTCCGTTTCATATACTTCAATATAAATATTATTAA  
 GTACTACAATTTGAAAACATCTTTAAATATACAACATATTTTGAATTAAGTTTA  
 TTTTTTTTTTTAGCCACATAGAGACATCTTTGTGGCATGCTAAATTCTGTAGTA  
 20 AAACCTTTCTTGGGGAAAGTGAAAGCCACGTATCAGACCAAAATCCACCCAAC  
 CCTGCACACACGCATCCCCATAAAGAACGACCTTGAGCT

**Genomic hit, Accession No.** CSC:AC014071

25 **Associated ORF**  
 Genscan ORF1 predicted sequences >16:36:33|GENSCAN\_predicted\_peptide\_2|477\_aa  
 MLILMRPSIKLAANQNAIKAPNGPKNFLDKVLVVRWLSVCLLENGHIAVTASGS  
 NNNNSNNINLNLKANYQMSATSIRDSFATILLDAQNRVQNATVAAKNFMLPLR  
 LRSDTSGDTSNNNENNSRRARQAYNCGVNWLTTHRPKRRRQVHPPLGSTPSCNN  
 30 NSSKISRNSSSSSNNIASATATRIFLGTSAILAIDFDNTRVPGYYQPTGEWIWVSKS  
 MIKQLFAVAATADDVAAAAASRGNALTFPLGKEKGPRKKAEGCGMEWSGVEWS  
 GGDVMCVLSSVATVDDDDHHGGGHFDGLLGTPSALIRLNCLINPKKMRMDFEVE  
 VAWQIARAADLRLISMHLNVPYEMKTMKTMESVIDGGSLYQPTALFGLFLCLVY  
 SSAADVLLLLANCKSLAHGVDVDCSDASRGSDCDVGHFSPSFRCRFQLSLVAQS  
 35 ARHANALKSQVTTATSSSSNNSDSLANKQTNQHIFVYQLSA

>16:36:33|GENSCAN\_predicted\_CDS\_2|1434\_bp

atgttgatcctaattgcggccgtcaatcaaatggccgcaaatcaaatgcaattaaagcgccaaacgggcccgaagaacttttga  
 caaagtcttggttgccgctgttgctgtctgtctgtctgcttgagaatgggcacattgctgtcactgccagcggcagcaacaaca  
 40 caacaacagcaacaacatcaacctcaattgaaagccaactatcaaatgtcagctacaagcatccgagattcggtcgccacgattct  
 tctagacgccccaaatcgagtgcacaaacgcaactgttgctgccccaaactcatgttgccgctgcgcctgcgcagtgacaccagc  
 ggtgacaccagcaacaacaacgaaaacaacagccggagagcaaggcaggctataattgtggcggttaactggtgacaacgcatt  
 cgccccgaagcggcggcggaagtgcacccgccttgggttcaacgcccagctgcaacaacaacagcagtaaatcagcagaa  
 acagcagcagcagcagcaacaacatgcacatcagcaacagcaacacgcattttcttggaacttcgcgattctggccatcgacttc  
 45 gacaatacacgagtaccgggggtattatcagccaactggggagtggttgggtatccaagtcctatgattaagcagctgttgctgtt  
 gctgccactgcggatgatgttgctgtctgtcagcttcacgcggcaatgcgttgaccttttgcgggaaaggaaaggggccaa

g g a a a a a g g c g g a a g g g t g t g g a a t g g a g t g g a g t g g a g t g g a g t g g c g a t g t g a t g t g t g c t c t c g a g t g t g  
g c c a c a g t t g a c g a t g a t g a t c a t c a t g t g g c g g c c a c t t g a c g g c t t g t t g g a a c a c c t t c a g c g t c a t c c g a c t t a a c t g c  
t t a a t c a a c c c g a a g a a g a t g a g g a t g g a c t t g a g g t t g a g g t t g c a t g g c a a a t t g c t c g a g c t g c t g a t c t g c g g c t g a t c t c a  
a t g c a c c t t a a t g t g c c t t a t g a a a t g a a a c g a t g a a g a c g a t g g a g a g c g t g a t c g a t g g t g g c t c c c t g t a c c a a c c g a c t g c  
t c t c t t c g g t t c t t t g t t t t g c t t g g t g t a t t c t c a g c t g c t g a t g t g t t g t g c t g t g c g a a c t g t a a a a g c t t a g c c a t g g c g t c g  
a c g t c g a c t g c g a c a g c g a c g c t a g c c g a g g c a g t g a c t g c g a c g t t g g c c a c t t t t c g c t t c g t t t c g c t g t c g t t t c a g t t g t c  
t c t g t t g c t c a a a g c g c g g g c a c g c g a a c g c t c t g a a a t c c a a g t t a c a a c a g c a a c a t c a a g c a g c a g c a a c a a c a g t g a  
t t c g t g g c a a c a a a c a a a c a a c a a c a t a t t t t g t g t a t c a a t t g t c g g c c t a a

- |    |   |   |
|----|---|---|
| 10 | <b><i>Drosophila</i> Gene Hit</b>                                 | rescue sequence, ORF1 and genomic sequence: Canton S E78B nuclear receptor superfamily protein (U01088)   |
|    | <b><i>Drosophila</i> EST</b>                                      | LP11082 (AI296953 similar by BLASTN to U01088)  |
|    | <b>Annotated <i>Drosophila</i> genome genomic segment</b>         | AE003593  |
| 15 | <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b> | CG18023 - Eip78C<br>Ecdysone-induced protein 78C<br>nuclear receptor NR1E1                                |
| 20 | <b>Human homologue of Complete gene candidate</b>                 | CG18023- 4e-32 119100<br>P20393 EAR1_HUMAN V-<br>ERBA RELATED PROTEIN<br>EAR-1<br>>gi 1082832 pir  A32608 |
| 25 |   |   |
|    | <b>Putative function</b>  | ligand-dependent nuclear receptor , putative transcription factor   |
|    | <b>Confirmation by RNAi</b>                                       | Not done due to failure of PCR procedure  |

**Example 14 (Category 1)**

<b>Line ID</b>	876/2
<b>Category</b>	Meiotic defects in testis: cytokinesis defects
5 <b>Reversion</b>	?
<b>Map Position</b>	73A
<b>Rescue ID</b>	2H1E
<b>Rescue Sequence</b>	
10	GATCAAACAGAAAAATCCAAAAACGAACAGCGCGCGGCGAACGAGAGCCGTT
	GAAGCCGCGCAGAGAAGTGCCTGCTCGCTCGCTGCCGGTATGTGCGTGTCTG
	TGCACTGAGAGAAAATGCTCGATTAAACAGAGAAATTAATAGTAATATAAAA
	AAAAAAAAAAATTTGTTTATTATTCTCAATTCAATAAAATGTAATTATTTATTAT
	ATTGGTTGTATAAGAATTTTATAAAGTAGTATAAATTTTCAATCAAATAAAT
15	ATGTACATCTAACAAAAAATGTTATTATCTTATAACAAAGAGGTAAAATCATA
	AGTAGTACGAAATCTTTAAAAGAGAAAGTGTGTTACGCAAAAAGTATTCAA
	GCAGTCTTTTATTTAATTTAATTTAATTTATTTGTGCTTTATCCCTTATATATATA
	TGACATTTTCATTAAAGCTAATGGTATAATTAGGTATTTACAGTGTTTAGCTAA
	GGCTTTCATCTGAAATATTTATTAATTATGTCTAGTTGACCTGTTTTTAGTTTTT
20	TTGNATAACAATATTTATTATTTATTAAGGAAAACAAGGGGAGAAGAAAAAC
	CTTAATTGAAGCAAAGCAGTCTTTTGAACCCACTGGTG
<b>Genomic hit, Accession No.</b>	AC005633
<b><i>Drosophila</i> Gene Hit</b>	rescue sequence: argos (M91381)
25	
<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003527
<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG10162 – Egf2 translation facto
30	
<b>Human homologue of Complete gene candidate</b>	CG10162 - 4e-11 181969 (M19997) elongation factor 2 [Homo sapiens]
<b>Putative function</b>	Translation elongation factor
35	
<b>Confirmation by RNAi</b>	Not done due to failure of PCR procedure

**CATEGORY 2: FAILURE TO ENTER M-PHASE****Example 15 (Category 2)**

5 **Line ID** 1216/12  
**Category** Meiotic defects in testis: no division  
(no meiosis)  
**Reversion** NR  
**Map Position** 82F1-2

10 **Rescue ID** 2I5X-1  
**Rescue Sequence 1**  
AAACCAAGCAACAGAAATATCTCCAGTAGAGAGCGCCACTGGAAGATCGGAA  
TTTTAGTGCTCTGCTCTGACTAACAGGTTTTAGTAGTAGTGCTTACTTTTCTAC  
TACGATTTTTGTGCGGGCTAACAATTCTGTTTTCCCACTCCCTCTCTCAGTTTTT  
15 GCATGGTAACTTTTCGGTCATTGTACTGTTGTTGTTGTCTTGCACACCGCAAGA  
GAACAACAACAATCGGAGAAACACTGATAGCGCGGTACAGTGGGGCAGGCCA  
AACTAGAACCTATACATTTAAGATGTCTCCAATTTGTGATTTTGCCTTTCAAGC  
ATACTAGTTCATAGTTGATTGTTTTGTTATGTTTTGTCTTGAATGCGATGTTTCA  
AGAAATCTTATTTTCGAATTACGATATTATTCTTATTCCTTTGACTTATTAATA  
20 TAAATGAAAACGGCGAGTAGAGCAAAAGAGCGACCACTGTGGCTCCACAAGC  
TCGTTTCTCTGTTTCTCATTTCGCGCCAGCTCCAATTTTCGCCTTATTCACACACA  
CACCTCACTGCTTGCGACTGCAAATTTGTGCAGCTGAACTTTG

**Rescue ID** 2I5E-1  
25 **Rescue Sequence 2**  
CTTGTTTATCACCTCTCTCTCTCTATCGCGCGCGCGCTCTTTGTGGAA  
ACAGGTATAACTGTTTGGCGTGAGGGAGCACGAAACTCCAGTGGAGACTTCTC  
CGCATCGCCAGCGAAACAAACGATCAAAATGAATACTCTGATAACGTGTGAA  
GGTGAGCAACAAAATAAAGTATAAGAAAATACCGCCACGAAAACAACAACA  
30 ATAGAAATGTCGACGCACCCTTTTCTTTTTCTCGCAAAGAACGAGGAAATGGA  
GAAGCGCAAAACCACATCCCGCTTAAAGAGTCCCTTTCCCCCGCTGGAAGTGG  
AAGGAAAGGCAGCTTAAAGAGGAGCGGGTGGCTTCCAGTATGTGGAAAACAA  
AGCAGACGCCATTGGAATGCCGTCGTTTTTGTGTTGCTAAGCCGGACATGG  
CAATTGTTGCTTTTGTTCGAGAGGGGGTGGTGAACTCATAAATATCAGCT  
35 ATGGCGAGGGGGTGGGGGCAGTCTTTGTCTGACGTACCGTACTTTTAATTTCTT  
GTCGCCCGGTTTAATCCAATTTATCCAGCTTTGAATTTTCGCGG

**Genomic hit, Accession No.** AC007532

40 **Annotated *Drosophila* genome genomic segment** AE003603  
**Annotated *Drosophila* genome Complete gene candidate** CG1116 - novel  
**Human homologue of Complete gene candidate** 2495728 HYPOTHETICAL  
PROTEIN KIAA0258(aa)

**Putative function**      No homologies which indicate function

**Confirmation by RNAi**      Slight loss of G1 peak

**Example 16 (Category 2)**

<b>Line ID</b>	1344/15
<b>Category</b>	Mitotic defects in brain: no mitosis
5 <b>Reversion</b>	NR
<b>Map Position</b>	83C
<b>Rescue ID</b>	2F6E
<b>Rescue Sequence</b>	
10	AGCGGGAGTGAGCCGAAAGAGAGTAATTTTGGCCGTCACCAAAAAAGTGGCT
	GCATAGTGCCAAACCAATGTATGGCCGTTACGCATCTTGTTATTCTAGTGTCTT
	TGGCTGTAATCAGTTTGCAGTGACAGAGGAGTTCAGTTTCAGTTGACTCGGCT
	TGGTTCAGGGTTTCTGATTGCCGTCCTCTTCTCCCTCTTCGCCTACAAGTCCGC
	TGTTCCGCACCGTGACGTCACCTAGACTTACACCCCTAATCAAAGATCCACTA
15	GTTTAGATTTCTGTCATCAACGCCATATTAACCTTTATAAGCAGTCGTTATATCT
	CAAGTAGGCAAAAAAGTGTAATAGATATGTATCTAAATTGTCGTACATTCTAT
	TTATTAAAATTCGTTTTTACATCCAACAGGTGTTATTTTTGAAGTCTTAGATAA
	CAAACAATATTCGAATTATGTGGTAGAATACTTAGCAATATACGCACATACAT
	ATACATATGAACATTATATCCAATGCTTTAAAACCGGAATATCAAGACAACAT
20	AATGCAACATCTGGTCCGAGCTATCCAGGCAATCACATTTTGAAGTTCCCCC
	GGTTATCACACATATATCGATCATACCCCGAAATGTGTAACACAGATACAGCT
	CACCATCCCTCTGATAAGATCTTATCAAGTTCGGGCTTGCTCGCTATCGTGAAT
	TGGGTTGAAGGGTCCGCGATAATTGCATTGGGCATGCCATTGGTAATCACAAT
	TGGCTGATAATGCTGCTGCTGCAATTCACGGGTATGAA
25	TTCATCAATTGGTTA
<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003602
<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG1347 - novel protein with myosin homology
30	<b>Human homologue of Complete gene candidate</b> 1503990 [dbj BAA13194  (D86958) KIAA0203 similar to mouse CC1.(aa)
35	<b>Putative function</b> similar to coiled coil protein with ubiquitin like domain
<b>Confirmation by RNAi</b>	Marked reduction of G1 and G2/M indicating fewer cycling cells
40	

**Example 17 (Category 2)**

**Line ID** 703/16  
**Category** Meiotic defects in testis: segregation defects, meiotic failure (Mf-07/75)

5 **Reversion** R  
**Map Position** 83B

**Rescue ID** 2E7E

**Rescue Sequence**

10 AAGCAGCCCCAACAGCTACGCAAAAAGTTACTTATATTTCGCAGCAAAACAGAT  
TTTTTGTTTTAATCGTAAGTATAGGAGTGAAAAATAGCGCTAGAGTAGACCT  
AAGTACACAGAAAGACAAATAGGGCGAGTAAAATCGCGGTCCTGGTCATTTC  
TCTGGCCTTGACCAATCCTTTGTCTGCGCTTTCGTTGGAAAAGGGGTTATGTAC  
GAAGTGCCTGCGTACCTAAGGCCAGATTAGTCATCGGGCAGTCATATATTCAT  
15 GCAAAAAATCATTGTTGGTGGCCGTCGGCCTTTGTTGACTGTACCTTGCTCATT  
TTTAATAAGCGCGACAGCAATATACACACTTTGAACCCCCATCCCACATTTTTT  
CTCACCGTTTCCCCCTAATTTTCGTTTTCCCTGTGCCCATCATTCGCTTTTCGCC  
ATGTCAGTGTATCGCTTCAAAATGGCGCCGAACCACATGTCTTCGTTCTCGGC  
TCGTCCGCTTCGTTTCGTGCGCTCGTGTGTGCTCTCATTCGCTCTCCGAATTCG  
20 TTTAACAAAGTGGTGCAGAGCAGAGGGGCCGCTGGATTTCGAGGCAAACAACAC  
ATATACCTA

**Genomic hit, Accession No.** CSC:AC013960

25 ***Drosophila* EST** several including LD15903 (AA440858), GH20091 (AI389018).

**Annotated *Drosophila* genome genomic segment** AE003602

**Annotated *Drosophila* genome Complete gene candidate** CG2922 – novel

30 **Human homologue of Complete gene candidate** 286001 dbj|BAA02795| (D13630)  
KIAA0005 [Homo sapiens] also  
NP\_054757.1| HSPC028 protein  
[Homo sapiens] e-179

35 **Putative function** Weakly similar to a region of human and murine  
EIF4G2 translation initiation factors; may act as a  
translation initiation factor

**Confirmation by RNAi** Only wild type profiles observed

**Example 18 (Category 2)**

<b>Line ID</b>	741/3
<b>Category</b>	Meiotic defects in testis: segregation defects, meiotic failure (Mf-05/31)
<b>Reversion</b>	NR
<b>Map Position</b>	88D
<b>Rescue ID</b>	H6E
<b>Rescue Sequence</b>	<p>GCCTGGAGCCACCTCTAGAGCCACGGCCAAAAAATTGTGTGCCAAAAAATCG  TATGGCGTTACGCATCTTGTATTCTAGTGTCTTTGGTTCTACAAATCTGGCCA  ATGGGATGGACGGATTTTGGGGCTTTTGCGCCCCACATATGTNTCTTACAACC  CACTCGGCCCCGGCAAGTGGGTGTCAATTACGGACATCGGCAATCCGAAGACC  GGAGACCCAGAGACCCTCAGACCCCAGGGCCCCATTCGATTTCGATTTCGAGTT  GCGTGGGCCGATCTCACATTAGTCACATCGAAGGAATGAAATAAAAAGAAAA  AACATGACGGCCGAAAAGAACTTATCCATCTTCAAAGCTCTCAGAAAATACA  AAAAACTAAAAAACTTTTGACTCTTCGTCTTTCACATTTTCGAAATCACAAAAT  GTCTGCCATAAATTCCAAAGTGAACAATTGAAATAAATTTTTCGCCCATGAAC  ACGCCGACTG</p>
<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003705
<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG12600 - novel protein
<b>Human homologue of Complete gene candidate</b>	<p>CG12600- 5e-27 4240227  dbj BAA74892.1  (AB020676)  KIAA0869 protein [Homo sapiens]</p>
<b>Putative function</b>	putative cytoskeletal structural protein
<b>Confirmation by RNAi</b>	Reduction of G1 and G2/M peaks indicating fewer cycling cells

**Example 19 (Category 2)**

<b>Line ID</b>	773/1
<b>Category</b>	Meiotic defects in testis: cytokinesis defects, meiotic failure (Mf-02/15)
<b>Reversion</b>	R?
<b>Map Position</b>	83F
<b>Rescue ID</b>	2D9P
<b>Rescue Sequence</b>	CCACCGCCCATGCCGCCATTTATTGAAAGGCCTGTACGCAGTTTGTGTTTTGTTT TTCTCTTTTTTGCTAGCTCAAACACAAAATTACTTTTTGTGGCTTGACTGGTGA GGTCTCTCTATCTCGCTTTTTTCGTCTTTACCTCGCTCTCATTCCCTCTCTATCTG CCCTGCTTCCTCTCACTATCTATCTACAACCTGAGGTCAACAAAATAAGTGCGT AGTCAAAAATGTAATTGAATTGATTGACAAACACAGCGAACGTAAATTTCCGT AATGTTTAACCTTGAATTCAAATGAACAACCTGTATAAATATAATACACGGGT AAACTCCATTTCAAAGCAAGCTAAAACATTTTAAATACATTTTAGGGAAACGG CCAATTAAGAATAATATTGTGGGGATCAATCTGGGGAAAAATGCAGTATC AGTAATGCTGAATATTTATTTTACTAAATTACAATGAAATGTCTCAAACAAAT GGGTTAATCATTTTCTTGCTCCATCTGCTTTTCCCAACTGTATCCAAGTACAAC TACAGCATTATCCTCAACTG
<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003675
<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG10272 - novel protein
<b>Human homologue of Complete gene candidate</b>	CG10272 - 2995577 AC004490 (AC004490) R29381_1(aa) protein includes HMG-I and HMG-Y DNA- binding domain (A+T-hook) found in HMG non-histone components in chromatin
<b>Putative function</b>	Chromosomal protein
<b>Confirmation by RNAi</b>	Loss of G1 peak indicating arrest in G2/M

**CATEGORY 3: METAPHASE ARREST****Example 20 (Category 3)**

5  
**Line ID** 1067/13  
**Category** Mitotic defects in brain: prometaphase arrest  
 (overcondensation, polyploidy, scattered chromosomes with  
 bipolar spindle)  
 10 **Reversion** NR  
**Map Position** 69C4-10  
  
**Rescue ID** 2F8E  
**Rescue Sequence**  
 15 GTTTGGGCACAGGGTTGTATTTCAATTTATTTTTGGGGGGAGTCGATACGCTCTC  
 TTGGCGTGGTTCGAACGGTCACACTGGCCGAGAGATAACGGAAAATGTTTCAA  
 AGGTAAGTAAAGATTATAAACGTATTAAGCTTAATACTATAATTAGCTTACTA  
 TTCCAAGTATGTATAATTATTACACGTTTAAAAGGCATAACGTTAAGTGTAAC  
 CAAATTATATCAATGGATTTTGAATACCAATATTATTTATTTTATATTTTGAGC  
 20 TTAATATATTAATCACATATATTTAAGCCTCTTTATATATGTAAATATTTTAA  
 TTTTATTAATAAATTATATATTGTTTTGTAAATATGATCGAGGGCTGCCACCT  
 TGTGATAAATGCTTACCAACACTTTTAGGTACGCCGTTTAGTGTACGTAAGTTG  
 CGTACCTAGATATCCAGCGAAATCAAAACATTGAGTAAATCGTGGAATAATGG  
 ATGAAAATAGCTTAATCTACGGAAGTGCAGGCGCGGGCTTTAACACCT  
 25 CAGTACGAGAGAGCAACGATGTGTGCTTCTTCATAGCCACCAACTCCTTGAA  
 GCCCACC AATCAGGTTCACTTAATCCAGTACGAAGA

**Genomic hit, Accession No.** CSC:AC020333

30 **Associated ORF**  
 Genscan: ORF1 predicted sequences: >16:51:11|GENSCAN\_predicted\_peptide\_2|178\_aa  
 MAQNISPEQSGGAGGGGSKHSDDSMVPKDNHAVSKRLHKELMNLMMANERGIS  
 AFDGENIFKWVGTIAGPRNTVYSGQTYRLSLDFPNSYPYAAPVVKFLTSCFHPNV  
 DLQGAICLDILKDKWSALYDVRTILLSIQSLLGEPNNESPLNAQAAMMWNDQKEY  
 35 KKYLD AFYEKHKDT

>16:51:11|GENSCAN\_predicted\_CDS\_2|537\_bp  
 atggcgcagaatatcagccccgagcaaaagtggaggcaggcggcgaggcagcaagcacagcgatgactccatgcccggtg  
 aaagacaatcacgccgtgagcaaaagactgcacaaggaactgatgaacctgatgatggccaacgagaggggcatctcagcgtt  
 40 tccggacggcgagaacatctcaagtgggtgggcaccatagcgggtccacggaacacgggtgtattcggggcaaacgtatcggtt  
 gtcactggattttcccaattctatccgtatgcagcacccgtggtgaagttcctgacgtcctgcttccatcccaatgttgatctgcagg  
 gcgccatctgtttggacatactgaaggacaaatggtcggccctgtacgatgtgcgcaccattctgctgtccatacaatccctgctgg  
 gcgaaccgaacaacgagagtcactgaatgcgcaggccgcgatgatgtggaatgac

- Drosophila* Gene Hit** TBLASTX with ORF1: poor homology to several sequences including homolog of RAD6 (DHR6) (M63792), bendless (L20126 ) and Ubc D1 mRNA for ubiquitin-conjugating enzyme (X62575).
- 5 **Human Homologue** TBLASTX with ORF1: ubiquitin carrier protein E2-C (UBCH10) (NM\_007019.1) and ubiquitin-conjugating enzyme E2B (RAD6 homolog) (NM\_003337.1 ).
- 10 **Annotated *Drosophila* genome genomic segment** AE003541  
**Annotated *Drosophila* genome Complete gene candidate** CG10682 – vihar ubiquitin-conjugating enzyme
- 15 **Human homologue of Complete gene candidate** gi5902146  
 0B6F58A1F0665D9A  
 |ref|NP\_008950.1| ubiquitin carrier protein E2-C [Homo sapiens] (2.50E-50)
- 20 **Putative function** Cyclin specific ubiquitin conjugating enzyme
- Confirmation by RNAi** Complete loss of G1 and G2/M peaks indicating fewer cycling cells. Immunostaining shows metaphase arrest with condensed chromosomes
- 25

**Line ID** 1105/1  
**Category** Male sterile, Female sterile, Mitotic defects in brain: prometaphase arrest  
 (Overcondensation, polyploidy, fewer anaphases, high mitotic index, scattered chromosomes with bipolar spindle)  
**Reversion** R  
**Map Position** 69C

**Rescue ID** A5B

**Rescue Sequence**

GTACATATAATCACAATTGAGAATCGAAAACCCGACCGCCACGAAGCGCGCT  
 AAATTACACGCACATACTGAAAGCCAAACAGCGGATAGCACTAGCATCCTAC  
 ATATATAGACGTAGATATATAGTCATGGCGCAGAATATCAGCCCCGAGCAAA  
 GTGGTGGAGCAGGCGGCGGCGGCAGCAAGCACAGCGATGACTCCATGCCCCGT  
 GAAAGACAATCACGCCGTGGAGCAAAAGGTGAGTATCACATGGTGCAGCCTA  
 AGATAATCCGCCAATATACACACACACTCACACTACCCACAGACTGCACAA  
 GGGAACTGATGAACCTGAATGAATGGGCCACCGAAAAAAGGGG

**Rescue ID** A5E

**Rescue Sequence 2**

ATATGTACTGTATAGTGGAATTTAGTTTGATCGGTCGGAATACGCGTCTGTT  
 GCTTTTTTCAGATATTTTTTTTTTCACTTTTGTGTGAAAACAAAATGGAAGGAGA  
 ACGAGAAGAACTGTGTTTGGGCACAGGGTTGTATTTTATTTTGGGGG  
 GAGTCGATACGCTCTCTTGGCGTGGTCGAACGGTCACACTGGCCGAGAGATAA  
 CGGAAAATGTTTCAAAGGTAAGTAAAGATTATAAACGTATTAAGCTTAATACT  
 ATAATTAGCTTACTATTCCAAGTATGTTATAATTATTACACGTTTTAAAGGCA  
 TAACCGTTAAGTTGTTAACCCAAATTATATCAATGGATTTTGAATACCAATATT  
 ATTTATTTTATATTTTGAGCTTAATATATTAAATCCACATATATTTAACCCCCCT  
 TTATATATGTTAAATATTTTAATTTTATTAAATAAATTATATATTGTTTGGTTA  
 AAA

**Genomic hit, Accession No.** AC007328 69B-69C

**Associated ORF**

Genscan: ORF1 predicted sequences

>/tmp/aaaaanjda|GENSCAN\_predicted\_peptide\_1|357\_aa

MGKKAKHKKKKGKGEKTKAMKADKKQAAARQKKMLEKLGEANIADIIQLLEAKEG  
 KIEAISESVCPPTPRSNFTLVCHPEKEELIMFGGEL YTGKTTVYNDLFFYNTKTV  
 EWRQLKSPSGPTPRSGHQMVAVASNGGEL WFPNFACISRNQSWFVFHNCRLKAA  
 SREKVLLNFNGTVLHPANNIIVHVKLFKKANGFKPWLLDVKLDACRFVRTNFHPF  
 VRIIFDLFKDFSTINHTCPYVVLRSRMRYIVRRSPRLVHPIVDVPAIGHTRPRRKA  
 AVRGIGCAHRCPLIRMATPCRTNVMMTLMRGSVRSRVMAICCYRRPAIAIARRRHP  
 TAIHSQEVAERLGGLLYPDIQRTNP

>/tmp/aaaaanjda|GENSCAN\_predicted\_CDS\_1|1074\_bp

atggcgcaaaaaggccaacacaagaagaaggcgcaaggcgccgagaaaacggccatgaaagcggaacaaaagcaggcgg  
 cgcgcgcaaaaagaaatgctggaaaaactgggagaagcaaatatagctgatcatccaattgctggaggccaaggagggaag  
 attgaagccatcagtgaatccgttggcccgccaccaactccacgatccaatttcaccttagttgccaatccggaagaggagctc

atcatgtttggcggcgaactgtacactggcacaaaaaccacagtgataacgatttgtctttacaacacaaaaccgtcgagtgg  
aggcagctgaaatgccatcgggacccacgccagaagtggacacaaatgggtgctgtggccagcaatggaggagaactct  
ggtttccgaacttcgctgtataagtcgcaatcaatcctggttgtgtccacaattgtcgtctgaaggcggccagtcgtgagaaggt  
cttactcaactttaatggaacggttctacatcggccaataacataatagttcacgtcaagctgtttaaaaggccaacggtttaagc  
5 cttggttattagacgtaaaactcgatgcttgtcgcttgtgcggaccaacttccatccgtttgtacgcattatattcgatctctcaaagat  
tttccaccataaaccacacgtgcccatatgtggtcctccgatcgatgcggtatattgtccgccgatccccacgacttgtgcacccc  
atcgtagatgttccggctattgggcacactcgcctcgacggaaggccgcgcttcgtggcatagggtgtgtcatcgctgccctct  
gattcggatggcgactccgtgtcgtaccaacgtggtgatgatgacgctgatgaggggctcggtgagatcgagggtgatggcgatt  
10 tgcgtctaccgccgaccgccattgccatagcccgctggcgccaccccactgccattgccactccaagaagttgctgaacgc  
ctcggtggtcttctttaccggacattcagagaaccaatccgtag

*Drosophila* EST      several ESTs including LD04777 (AA201675)

All other entries as for 1067/13.

**Example 21 (Category 3)**

	<b>Line ID</b>	1407/13
	<b>Category</b>	Mitotic defects in brain: (weak overcondensation, metaphase with bipolar spindle)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	92B1-3
	<b>Rescue ID</b>	2D3P
10	<b>Rescue Sequence 1</b>	
	ATCACGAATTTGACATTGCTACCACATTCGGTGCGTGGACTCTGAAAGCTCTG AGTGT TTTGTTTATGCAAAGCTTTTTTGGACTATCGCGTGGTAAGTAGCCGAAA GAGAAAGCTCTCTTATACGGAAGATGAAGAGTGTGATTCATGAAAATGTATA AGAACGCGGGTCCAAAAAGTCAAGGGAGTTCTAGTGAAATGAAAAGTTCCAA 15 AGGTTTTGAAATCGTTTTATTTCTCGTTCGTATAATTATTGGGTGTCGATCTTT GTTGGGCAGTGTAAGCACAACTTTGAGCTTCATCATAACATATCATATGTAA AGCCGGGACGAAAGCTTATGATTCTGTAAAGTGTCCGCCCAAGATAACATTTT TCCAGCCCTTCAAATCTTCAAATAAATACGGCTTAAGGCGAGCAAATTTGTAA ATCAAATGATTTGTAAATAAACATTATATGTATTTTATCATGCCAGGTTAGAA 20 CACATTGTGCTGATGCAAATAAAATTCCAATTAACGCCCTGAATGGGAAGA TGACGCATCTTTAATGGGAATATTATGGTAAATTTAATA	
	<b>Rescue ID</b>	2D3E
	<b>Rescue Sequence 2</b>	
25	TNCGTGATTATCAGCGTTAATTGTACAATATTATGATTTATTCGAGCTGTAAAT CTTCACAGCAAGCACAACTGTAATTATACCACTTAGAATCCGCGGAATTAA TTCTTGAAGACGAAAGGGCCTCGTGATACGCCTATTTTATAGGTAAATGTCAT GATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCG GAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGA 30 GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAG TATTCAACATTTCCGTGTCGCCCTTATTCCTTTTTTGCGGCATTTCCTTCCT GTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTG GGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAG	
35	<b><i>Drosophila</i> EST</b>	LD05707 (AA246767)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003727
40	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG7444 - very short ORF with EF hand homology
	<b>Human homologue of Complete gene candidate</b>	none
45	<b>Putative function</b>	Possible calcium binding protein

**Confirmation by RNAi**      Slight loss of G1 peak

**Example 22 (Category 3)**

<b>Line ID</b>	1439/7
<b>Category</b>	Mitotic defects in brain: prometaphase arrest. (overcondensation, polyploid, no anaphases, scattered chromosomes with bipolar spindles)
<b>Reversion</b>	?
<b>Map Position</b>	96F10-14
<b>Rescue ID</b>	G3X
<b>Rescue Sequence</b>	GTCGGATGTAGAAGACGTGCCCCGAAACCCAGTTAGAAATCGATGTCAGCGAT GGCGCCGGACTGGAGGATGAGGATGATGACGATATGGAACAGATTACAGCTC AGAAGGTAAGGTAAATCGTAACAGAGCTTTTTAATACGCAAGTAATCACATTC TGATATCCCTAGGTTCTGGAAATCATAGAAACCGCGTGGATAAATGAAATGTG TGCGCCGGAGATCCTGCCCAGCCAGACGGACATGCTGGAGCTGATGGTCTCCC AGGTGGCCCATATGGAGGAGCAGATGCGCGATCTGGACAAGAACGATTTCCG AGCGGTGGTGCACCTCCATGGAAGTGGAGAGGGTGCCTACATAATGGCCAGT TATCTGCGTTGCCGCTGCAGAAGATCGAAACCTTCACGCAGCACATCCTCAA CCAGGAGGAGAGCCGTGAGCCGGATGACAAACGTCTGTCTCCCGAGGAGACT AAGTTCGCCCAGGAGTTTGCCAGTAAT
<b>Genomic hit, Accession No. AC007825</b>	
<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003754
<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG14549 – novel
<b>Human homologue of Complete gene candidate</b>	none
<b>Putative function</b>	no homologies which indicate function
<b>Confirmation by RNAi</b>	Only wild type profile observed

**Example 23 (Category 3)**

**Line ID** 1466/4  
**Category** Mitotic defects in brain: metaphase arrest.  
(overcondensation, no polyploidy, fewer anaphases, metaphase  
5 with bipolar spindle)  
**Reversion** NR  
**Map Position** 72F

**Rescue ID** E5E

10 **Rescue Sequence 1**

GGCTGGATGCGATTTCGCTTTCGGATTTCGGATTTCAGCCGCTGTCTCGACA  
CCGCCGCAACCGCTCTCGGGAGTTTGAAAATTTGAAATGAGCGGATTTCGCGTT  
GCGAAGGCGAGCTAGCGTTGCAGGCAGTGTGGCCAGATGCCGCGTGCGAACG  
TATTCTCGAATGCAATCGGCCGAGTGCAGATGCACTAAAAATAACCCACTTCC  
15 AGTGACTGGAAATTAAGATCAAGGNAATAGATTTTATAAAAACTTATATGAGT  
AAAAATTTTAAAAATTGTGGAGTCAACCTAAATTATAAGCAACTAATTTATAAC  
ACAAGTAAAGAATGATATTAAGTAACTTTTTAAATAATATTCCATTATGCTTA  
CGCTCAATTTATGAACAAATGTTTTCTCGATCCTTAGGTAAAGTTTCGAGTTTC  
GCGACTANATTTATTAAAATTAAGAACATCTCCATTTATGTACACATTTAAAG  
20 ATTTATGAGCGGTAATATTAGCTGGTTGAC

**Rescue ID** E5P

**Rescue Sequence 2**

ATCCAGCCAAGATATCCTATCGTGCAGCTGAAACCCGAAACCCGAATCCGAGT  
25 TCGAAACGAAACGAATCGCAGTGGTGGTTTCTCTCTCGCTCTCTAGCTCTCCCT  
CTCTCTCGCGTGTGTGTATGTGTGCGAGTGGCAGGAAAAGTGCGAAGCCGAAA  
TCTTTTTAGCTGAAAGAAAGCGCAACTTCAATTAGCGAAAAGCAAGAGTAGCT  
AACAAAAAGAAAAGCGGATCGAAAAGTAAAGAAAAACAAAAAACA  
AAAGCAACAAATCGAAATGGCAAGCGAAGTGGCCCAAATACCGCCGAGGG  
30 AACGCCCCGAGTGGCGGCGGCGGAAAAATCAGAGGAGCCGGAAAAGTCAG  
CGGCCCCGCCAGCGGACTCAGCGGCCGCTCCAGCTGCCGCCCCCGCAGTGGA  
GAAGGCTGAGGATGCCGATGGCGAAAAAAGGACGGCGAGGCCGGAAAAGCA  
GGACAAGCAGCAGGATGGC

35 **Genomic hit, Accession No.** CSC:AC020154

**Associated ORF**

Genscan ORF: ORF2 predicted sequences

>21:06:03|GENSCAN\_predicted\_peptide\_5|415\_aa

40 MASEVAQIPAEETPAVAAAEKSEEPKSAAPPADSAAAPAAAPAVEKAEDADGE  
KKDGEAGKQDKQQDGEEPKKDEAVAAPVATKSEAPPAQKFNVHKTNFEKDIIYL  
YQFSRTPLLPSLSPYCLKVETWLRLVGLKYENVDHKMRFRSCKKGQLPFIELNGEEI  
ADSAMIKELSSKYEKYLDSGLTAEQRNVSYATIAMLENHLIWIIFYWRAKYPDNV  
LKG YKVN LQHALGLRLPNSILNFFFKITFGRKGTKKLKAHGIGVHSAEEIEEF GKD  
45 DLKVLSEMLDCKPFFFGDEPTTLDVVAFAVLSQLHYLSKDIA YPLRDYMT EKC PN  
LIGHVSRMKDKCFPDWDEICTKL DLNAHIPKPEPETKEGKEGGEQEKSNEQEGTE

GDKIEKELEKDKSNEKESTEENKEKEETK

&gt;21:06:03|GENSCAN\_predicted\_CDS\_5|1248\_bp

atggcaagcgaagtggcccaataacccgccgaggaaacgcccgcagtggcgggcgcggaataatcagaggagccggaaaa  
 5 gtcagcggccccgccagcggactcagcggccgctccagctgccgccccgcagtggagaaggctgaggatgccgatggcga  
 gaagaaggacggcgaggccggaaagcaggacaagcagcaggatggcgaggagcccaaaaaggacaggcggtggcagc  
 acccggtggcgaccaaatcggaagccccgccgcccagaaattcaatgtgcacaagaccaactcgagaaggacatcatctatct  
 gtaccagtctcgcgcacccactgtgccctccctgtgccctactgcctgaagggtggagacctggctgctctgtgggcctga  
 aatacgagaatgtcgatcataagatgctgttccgctccaagaagggtcagctgccgttcacgagctgaatggggaggaaatcgc  
 10 cgattcggccatcatcatcaaggaaactgtcgtccaaatacgagaagtacgtggactcgggactcaccgccgagcaaaaggaatgt  
 ctgtagccacgattgccatgctggagaaccatctcatctggatcatcttctactggcgcccaagtatccggacaatgtgctcaa  
 gggctacaagggtcaacttgtagcagcgcctcggcctgcccactcgattctgaacttctttaaagatcaccttggtcgc  
 aagggcacgaagaagctgaaggcgcacggcatcggtgtccacagcgcggaggagatcgaggagttcggcaaggacgacctg  
 aagggtgctcagcgagatgctcgactgcaagccttcttctcggcgacgagcccaccacctggatgtggtggccttcgctgctct  
 15 ctgcagctccactatctgtccaaggacattgcgtatccgtgcgcgactacatgaccgagaagtcccccaacttgattggccacg  
 tatctcgatgaaggacaagtgtctcccgactgggacgagatctgcacgaagtggacctcaatgcgcacattcccaagccag  
 agcccagagaccaaggaggggaaggaggggtggcgagcaggagaaatcaaacgaacaggagggcactgagggcgacaagat  
 cgagaaggagttggagaaggacaagtcaaacgagaaggagtcgaccgaggagaacaaagagaaggaggaacaaagtaa

- 20 **Drosophila Gene Hit** rescue sequence and TBLASTN with ORF2: failed axon  
 connections (U21685)  
**Human Homologue** BLASTX with fax: Metaxin 1 and 2 (Q13505 and AF053551)  
**Drosophila EST** several including LD31362 (AA951078 similar by BLASTN to  
 U21685 failed axon connections)

25

**Annotated Drosophila genome genomic segment** AE003527

**Annotated Drosophila genome Complete gene candidate** CG4609 – fax failed axon  
 connectionsconnections

- 30 **Human homologue of Complete gene candidate** 4505281  
 ref|NP\_002446.1|pMTX|  
 metaxin>gi|3024205|sp|Q135  
 05|MTXN\_HUMAN  
 METAXIN (4e-06)

35

**Putative function** Drosophila fax is a dominant genetic enhancer of the Abl mutant,  
 developmentally expressed in axons of the CNS

- 40 **Confirmation by RNAi** Weak reduction of G1 and G2/M peaks indicating fewer  
 cycling cells

45

**Line ID** 262/20  
**Category** Mitotic defects in brain: metaphase arrest.  
(overcondensation, polyploidy, aneuploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle)  
5 **Reversion** NR  
**Map Position** 72F

**Rescue ID** G6E

**Rescue Sequence**

10 AGCTGCACGATAGGATATCTTGGCTGGATGCGATTCGCTTTCGGATTCGGATG  
GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA  
ATTTGAAATGAGCGGATTCGCGTTGCGAAGGCGAGCTAGCGTTGCAGGCAGT  
GTGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCA  
15 GATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAAT  
AGATTTTATAAAAACTTATATGAGTAAAAATTTTAAAAATTGTGGAGTCAACCT  
AAATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTT  
TTTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCG  
ATCCTTAGGTAAAGTTTCGAGTTTCGCGACTAGATTTATTAATAAATTAAGAACA  
20 TCTCCATTTATGTTCCC

**Drosophila EST** several including LD28084 (AA949260)

All other results as for line 1466/4

**Line ID** 262/22  
**Category** Mitotic defects in brain: metaphase arrest.  
 (overcondensation, polyploidy, few anaphases, high mitotic index,  
 metaphase with bent bipolar spindle)  
 5 **Reversion** NR  
**Map Position** 72F

**Rescue ID** F1E

**Rescue Sequence 1**

10 AGCTGCACGATAGGATATCTTGGCTGGATGCGATTCGCTTTCGGATTTCGGATG  
 GATTTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA  
 ATTTGAAATGAGCGGATTTCGCGTTGCGAAGGCNAGCTAGCGTTGCAGGCAGT  
 GTGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCA  
 GATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAAT  
 15 AGATTTTATAAAAACTTATATGAGTAAAAATTTAAAAATTGTGGAGTCAACCT  
 AAATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTT  
 TTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCG  
 ATCCTTAGGTAAAGTTTCGAGTTTCGCGACTAGATTTATTAATAAATTAAGAACA  
 TCTCCATTTATG

**Rescue ID** F1P

**Rescue Sequence 2**

GTGCAGCTGAAACCCGAAACCCGAATCCGAGTTCGAAACGAAACGAATCGCA  
 GTGGTGGTTTCTCTCTCGCTCTCTAGCTCTCCCTCTCTCTCGCGTGTGTGTATGT  
 25 GTGCGAGTGGCAGGAAAAGTGCGAAGCCGAAATCTTTTATAGCTGAAAGAAAG  
 CGCAACTTCAATTAGCGAAAAGCAAGAGTAGCTAACAAAAAGAAAAGCGGAT  
 CGAAAAGTAGAGAAAAACGAAAAAAAAAAAAACCAAAGCAACAAATCGAAATG  
 GCAAGCGAAGTGGCCCAAATACCCGCCGATGAAACGCCCGCAGTGGCGGCGG  
 CGGGAAAAATCAGAAGAGCCGGAATCAGCGGGCCCGCCAGCGGGACTCTG  
 30 CGGGCGCTCCAGCTGCCGCCCCCGCAGTGGAGAAGGCTGAGGATGCCGATGG  
 CGAA

**Drosophila EST** several including LD28084 (AA949260), LD38479 (AI518768)

35 Other results as for line 1466/4

	<b>Line ID</b>	262/3
	<b>Category</b>	Mitotic defects in brain: Metaphase arrest (overcondensation, polyploidy, aneuploidy, no anaphases, high mitotic index, metaphase with bipolar spindle)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	72F
	<b>Rescue ID</b>	H3E
	<b>Rescue Sequence</b>	
10		AGCTGCACGATAGGATATCTTGGCTGGATGCGATTCGCTTTCGGATTCGGATG GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA ATTTGAAATGAGCGGATTCGCGTTGCGAAGGCGAGCTATCGTTGCAGGCAGTG TGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCAG ATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAATA 15 GATTTTATAAAAACTTATATGAGTAAAAATTTTAAAATTGTGGAGTCAACCTA AATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTTT TTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCGA TCCTTAGGTTAAGTTTCGAGTTTCGCGACTAGATTTATTAATAAATTAAGAACATC TCCCTTTATGTTC
20		Other results as for line 1466/4

### Example 24 (Category 3)

5	<b>Line ID</b>	238/20
	<b>Category</b>	Mitotic defects in brain: metaphase arrest (overcondensation, metaphase with bipolar spindle)
	<b>Reversion</b>	NR
	<b>Map Position</b>	75E1-3
10	<b>Rescue ID</b>	D7E
	<b>Rescue Sequence</b>	TTCAGTCGCGCATTTACCGTTTCCGAATCGGACGAACCGGGCGTGATTGCTC TCCTGCTGCTTTCGAGATCGGAGTCCCGATAAGGATATAACTACAACCTAAAG AGGAATCCAAGCCTCCTCCTGCCGCTAGTTTCGAAAAGTAAATAGAGTACTTG TTATCAACTGGGGAAGCGGAGATACATAGCTCCGATATTCTGTGAAAGCCAG 15 ACAAACGGATACCAACGAACAATCGCCATGTGCGTCGTCGTCCCTTCTCGTTT CACACATCGTGCGATAAAAATAACCGCTTTGCTTTTTGTGTTTATTTAAAAATTT TGGTTAGGAAGTGAACCTCGAACTCGTGACGTTTGCATTTTCACAACAACAAAA AGAGCAAAACATAGCAGAAGAACCCCAAGAAACAGGAACAGAAACCGTT GACCGAGTGCCAGTGTGAAGGTCTAGGCACAAAGAACGCTACCAAGAACTCT 20 TGGGAGTTAGGGAGGCTCTTTACAATGACAACATTGCACCAAAGATGGACTCT CTCTCTAAAATGCATTTTCATACCAATATTTACTTT

***Drosophila*** EST several including LP04802 (AI260815)

25	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003519
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG3979 - novel gene with homology to sodium- dependent dicarboxylate transporters
30	<b>Human homologue of Complete gene candidate</b>	3e-87 4506979 ref NP_003975.1 pSLC13A2  UNKNOWN >gi 2499523 sp Q13183 NDC1 _HUMAN RENAL SODIUM/DICARBOXY
35		

40	<b>Putative function</b>	sodium/dicarboxylate transporter
	<b>Confirmation by RNAi</b>	Only WT profiles observed

45

**Line ID** 490/9  
**Category** Meiotic defects in testis: segregation defects, multipolar spindles (Mul-02/29)  
**Reversion** NR  
5 **Map Position** 95C1-8

**Rescue ID** I4E

**Rescue Sequence**

10 GCTCTGCCGCTTCAACCGCCCGCGTTCTGTGTGTTGGTGTGCCGCGACGTAGG  
TG TAGGGTCCGCTGCACACGTGTGTGTGGGAGCGCGCGAGAGCGGGAGAAGA  
GCAGAACGTTTTTTGGGCGGCTAGTGGTGGCACCGTGAGCATGCCGGTCGTCGT  
AAGATAGGCTTAGGAACACTCAGAGAAAATTTGTTTAGCTCAGCATTTTCCTA  
TTATTGAAATCATTTATTTGATGGTCTATGGGGGTTTCTTTTCGTAGTTATTCAT  
AGATCGGCGATTTAAGCTACGCTTAAAGGGTAATTTGTCTGAGATATCTTTGT  
15 CATTTAAAGTTAAGTCTCAGCTTATCCAAAAGTCAGTTATTGGAAAAAAGGAG  
CCAGCTTTTCAGCAGAGTTCGGCTTAAGCGCTTATTATCATATTAACCAGCTTA  
ATTAATGTATCTTTTAAATTGTTATATGCATTAAATCACTAATTAAGGTGATTA  
CCATTTGTACGTTTTTAAATTAAAGTATTTTGATTTTCACTAATACAGGCTCTAA  
20 GCTGATCCAAATCTACAAGCTTAGTTTTTGAATAGTCTTCACATGTTGACTTTT  
ATTCTCT

**Genomic hit, Accession No.** CSC:AC015160

Other results same as 238/20

25

**Line ID** 660/3  
**Category** Meiotic defects in testis: cytokinesis defects, abnormal spindles.  
(Ab-01/03)  
**Reversion** R?  
5 **Map Position** 75E

**Rescue ID** H8E

**Rescue Sequence**

10 GCTCTGCCGCTTCAACCGCCCGCGTTCTGTGTGTTGGTGTGCCGCGACGTAGG  
TG TAGGGTCCGCTGCACACGTGTGTGTGGGAGCGCGCGAGAGCGGGAGAAGA  
GCAGAACGTTTTTTGGGCGGCTAGTGGTGGCACCGTGAGCATGCCGGTCGTCGT  
AAGATAGGCTTAGGAACACTCAGAGAAAATTTGTTTAGCTCAGCATTTTCCTA  
TTATTGAAATCATTTATTTGATGGTCTATGGGGGTTTCTTTTCGTAGTTATTCAT  
AGATCGGCGATTTAAGCTACGCTTAAAGGGTAATTTGTCTGAAATATCTTTGT  
15 CATTTAAAGTTAAGTCTCAGCTTATCCAAAAGTCAGTTATTGGAAAAAAGGAG  
CCAGCTTTTCAGCAGAGTTCGGCTTAAGCGCTTATTATCATATTAACCAGCTTA  
ATTAATGTATCTTTTAAATTGTTATATGCATTAAATCACTAATTAAGGTGATTA  
CCATTTGTTTCGTTTTAAATTAAAGTATTTGAATTTC

20 **Genomic hit, Accession No.** CSC:AC015160

Other results same as 238/20

**Example 25 (Category 3)**

**Line ID** 273/18  
**Category** Mitotic defects in brain: metaphase arrest  
 5 (overcondensation, very high mitotic index, few polyploids, metaphase with bipolar spindle )  
**Reversion** NR  
**Map Position** 75E

10 **Rescue ID** D1E

**Rescue Sequence**

AACTGGGCTAAAACCAGCTGAAAAGTAAAATATTTGGAGAAG  
 GAAAGCCTTAAGTTCCTCTCTACGCTTCGTACACGTAATGTGCGTGTTTAATC  
 TACGTTAAACAAGTGGAACCATGTTACGTGCCGTGGCTTTGTGTGTGTCAG  
 15 TGGTGCTCATAGCACTATATACGCCAACTTCTGGGGAATCCAGTCAGAGCTAT  
 CCCATTACCACGCTAATCAACGCGAAATGGACGCAGACGCCCCTATATCTGGA  
 AATCGCCGAGTATCTGGCCGATGAGCAGGCGGGCCTCTTCTGGGATTACGTTT  
 CGGGGGTGACAAAGTTGGACACGGTTCTCAACGAATATGGTTTGTGTTTATAA  
 GTCATGGAGAACCCGCATTAAAGAGCTTTTATATTCTCCTCAATGTGAATCC  
 20 GAATCCATATAAAATC

**Genomic hit, Accession No.** AC015160

**Associated ORF**

Genscan: >ORF2 predicted sequences

25 >16:57:34|GENSCAN\_predicted\_peptide\_5|1548\_aa  
 MLRAVALCVSVVLIALYTPTS<sup>5</sup>GE<sup>5</sup>SSQSY<sup>5</sup>PIT<sup>5</sup>TLN<sup>5</sup>AKWTQTPLYLEIAEYLADEQA  
 GLFWDYVSGVTKLDTVLNEYDTESQQYNAALELVKSHVSSPQLPLRLVSMHS  
 LTPRIQTHFQLAEELRSSGSCQSFTFAQVGSELACSFNELQKKLEVPLAKDSL<sup>5</sup>SDAS  
 VVTYSFDHIFPGSENNTRTVVLYGDLGSSQFRTYHKLLEKEANAGRIRYILRHQLA  
 30 KKDKRPVRLSGYGVELHLKSTEYKSQDDAPKPEAGSTSDEDLANESDVQGFDFK  
 VLKQKHPTLKRALDQLRQRL<sup>5</sup>LQGN<sup>5</sup>DEIAQLKAW<sup>5</sup>EFQDLGLQAAAAIAEIQGD<sup>5</sup>ET  
 LQILQYTAHNFPMLARTLLAHKVTDGLRAEVKHNT<sup>5</sup>EAFGRSLNVAPPD<sup>5</sup>GALFING  
 LFFDADTMDLYSLIETLRSEMRVLESLSHNNVRGSLASSLLALDLTASSKKEFAIDI  
 RDTAVQWVNDIENDVQYRRWPSSVMDLLRPTFPGMLRNIRKNVFN<sup>5</sup>LVV<sup>5</sup>DAL  
 35 QPTARSVIKLSESFVIHQAPIRLGLVFDARDANEDNLADYVAITCAYNYVSQKKD  
 ARAALSFLTDIYAAVGETKVVTKKDIVKQLTKEFTSLSF<sup>5</sup>AKAE<sup>5</sup>EFLEED<sup>5</sup>STYDYGR  
 ELAAEFIQRLGFGDKGQPQALLNGVPMPSNVVTADSDFEEAIFTEIMTHTSNLQKA  
 VYKGELTDNDVAIDYLMNQPHVMPRLNQRILSQEDVKYLDINGVAYKNLGNVG  
 VLNRLSNRDMTATLMDNLKYFGGKKSTELIGRASLQFLTIWVFADLET<sup>5</sup>DQGRD<sup>5</sup>LL  
 40 THALDYVQSGESVRVAFIPNTESSASSRRNLNRLVWAAMQSLPPTQATEQVLK  
 WLKKPK<sup>5</sup>KEIEPTQLEDILG<sup>5</sup>STELHLKMLRVYSQRVLGLNKSQRLVIGNGRLYGPL  
 SSDESFD<sup>5</sup>SAD<sup>5</sup>FALLARFSS<sup>5</sup>LQYSDKVRQVLKESAQDVNEEFNSDTLLKLYASLLPR  
 QTKTRFKLPTDLKTDHSVVKLPKQENLPHFDVAAVLDPASRAAQKLTPILILLRQ  
 VLNCQLNLYLIPVPQHSDMPVKNFYRYVVEPEVQFEANGGRSDGPLAKFSGPLAN  
 45 PLLTQQLQVPENWLVEAVRAVYDLDNIKLTDIGGPVHSEFDLEYLLLEGHCFDAA  
 SGAPPRGLQLVLGTQSQPTLVDTIVMANLGYFQLKANPGAWSLRLREGKSADIYA

ISHIEGTNTHHSAGSSEVQVLITSLRSHVVKLRVSKKPGMQQAELLSDDNEQAAQS  
 GMWNSIASSFGGGSANQAATDEDTETINIFSVASGHL YERLLRIMMVSLKHTKSP  
 VKFWFLKNYLSPQFTDFLPHMASEYNFQYELVQYKWPRWLHQQTEKQRTIWGY  
 KILFLDVLFP LNVRKIIFVDADAIVRTDIKEL YDMDLGGAPYAYTPFCDSRKEMEG  
 5 FRFWKQGYWRSHLMGRRYHISAL YVVDLKRFRKIAAGDRLRGQYQALSQDPNS  
 LSNLDQDLPNNMIHQVAIKSLPDDWLWCQTWCSDSNFKTAKVIDLCNNPQTKEA  
 KLTAARIVPEWKDYDAELKTLMSRIEDHENSISRDSA VDDSVDDSV E VTTVTPS  
 HEPKHGEL

10 >16:57:34|GENSCAN\_predicted\_CDS\_5|4647\_bpatgttacgtgccgtggccttgtgtgtctgtggtgctca  
 tagcactatatacggcaactctctggggaatccagtcagagctatcccatcaccacgctaataacgcgaatggacgcagacgcc  
 cctatatctggaaatcgccagtagtatctggccgatgagcaggcgggcctctctgggattacgttctgggggtgaccaagttggaca  
 cggttctcaacgaatatgataccgagtcgcaacagtacaatgccgccttggagctggtcaagagccatgtgagttctcccaattg  
 ccctgcttaggtgtggttatccatgcatagttgacgccccggatccagaccacttccagttggccgaggaaactgaggagca  
 15 gtggtcttgcagagctttactttgcccaggtgggttccgaactggcctgcagctttaacgagctgcagaagaagctggaagtgc  
 cgctcgccaaggatagcttggatgcttctgtgtcacctacagcttggatcacatttccctggcagtgagaacaatacccgcaactgt  
 ggtactatacggcgatttgggaagctctcaattccgcacatcacaaactattggaaaaggaaagccaatgctggccggattcgta  
 catcttgcgtcatcaattggccaagaaggacaagcgaccggtagcactttcgggctatggagtggaaactccatctgaagtcaacg  
 gaatacaagagtcaggatgatgctccaaagccccgaagctggttccacttctgatgaggatttggctaataatcgacgtccagg  
 20 gctttgattcaagggtgctgaagcagaagcatcctacacttaagagagcgctggatcaactgcgtcagagggtcttccagggaac  
 gatgagatcgccaattgaaagcatgggagttccaggatttgggtctccaggcgccgctgctattgcagaaatacagggtgatg  
 aaacctacaaattcttcaatactgcccataatttccccatgttggccagaacctgctggccacaagggttacggatggcttaag  
 ggcggaggtaaagcataatacggaaagcatttggaaagcttgaatgtagcgctccagatggtgcccttttcatcaatggactctt  
 ctctgatgctgacacaatggatctgtatccctgattgagacgctgcgctcgagatgcgtgttctcgagagctctgcacagtaataat  
 25 gtgaggggaagccttggcagctccttgccttggatctgacggcctccagcaaaaaagaattcgccatcgacatccgtgaca  
 ctgcagtacagtggttcaacgatattgaaaacgatgtgcagtaccgcagggtggccctcatcggtgatggatcttttgcgtccaaact  
 ttctggcatgttaaggaaataccgaaagaatgtgtcaatttggctcctagtgttagacgcgctgcagcccacagctagaagtgttat  
 taaactgctagagtcgtttgtcatccatcaagctcccattcgttgggttgggttctgatgcgagggagccaacgaggataatcttg  
 cagattacgtagccatcacgtgcgcctataactatgtgagtcagaaaaaggatgcccgagctgctttaagtttctcaccgacatct  
 30 acgcagcagttggtgagaccaaagtgggtcacgaaaaagacatagtaagcaactaacgaagggaattacatcattaagctttgc  
 caaagcggaggagttcttggagggaagattccacgtacgactatggcaggagctcgcagcagagttcattcagcggctgggatt  
 cggagacaagggacaacctcaggccttgttgaatgggtgttccaatgccagcaacgttgtgaccgccgatagcgacttcgagga  
 ggctattttaccgagattatgaccacaccagcaatctccaaaggctgtgtacaaaggtaactgacagacaacgatgtagcca  
 ttgattatctgatgaatcaacctcacgtgatgccagattgaatcagcgaatcctaagccaggaggtgtaaatatcttgatattaac  
 35 ggcgtggcctacaaaaatcttggcaatgttggagttaaaatcgtctgtctaacgggatagaccgctacgctaataatgataatcttaa  
 atactttggtggcaagaagtctacggagcttattggccgagcatccctacagttcctaacgatttgggtgttctgatttggaaactg  
 accagggctgagatctgctcacccatgccctggactatgtccaaagtggagagagtgctgcagtgcaattcattccaacactga  
 aagctcttccgcctcaagccggagggaatcttaacgatgttgggtggctgccatgcagagcttccaccaactcaagccacggagc  
 aggttctcaagtggctaaagaaaccaaaggagaaaattgagataccactcagctcgaggatatcctgggatctacagagctgca  
 40 cctgaagatgttgagagtttattccagcgagtggttgggtctaaataaatccagcgttggctatcggtaatggcggttattggg  
 ccccttctgctggatgaaagctttagatgcgccgatttctgtttagcaggttcagttctctacagtatagcgataagggtgcgtca  
 ggtcctgaagggaatctgctcaagatgtcaatgagggaattcaacagcgatacattgcttaagttgtatgccagcctgcttccaggca  
 aacccaaactcgctttaaagctaccaacggacttaaaaaccgatcactcggttgaactaccgcccacaggagaatcttcccc  
 attttgatgttgcgcgcttggatccgcctccgagcagctcaaaaactaacgccaatactattttgcttgcgaagtgtgaaact  
 45 gccaatgaaactatactgattcccgctccccagcacagcgatatgcccgtaagaacttctacagatacgttggaaaccggag  
 gtccaattcgaggcgaatggaggccgatctgatggctcttggccaaactcagtgattgccagccaatcctctgctgaccagca  
 gctgcaggttcccgagaactggttgctgaagctgtgagagcagttacgatctggacaacattaagttgaccgatattgggtggac  
 ctgtgcacagcgaattcgatctggagatctgtgttggagggtcactgctttagtctgctagcggcgctccgccagaggacttc

agttgggtgtgggtaccagagtcaacctaccttggtagatactattgtgatggcgaatttgggttattccaactaaagccaatcca  
 ggagcttggtccctacgcttgcgtgaaggcaaatcggcggatattatgcaatcagccacattgaagggaacaaataccatcattc  
 ggctggctcttctgaagttcaggttcttataacctccttgcgatcccatgttgcaaatgaagggtgtctaagaagccaggcatgcag  
 caggcgggaactcctgtcagatgacaacgaacaggcagcgaatcaggcatgtggaacagcatcggcagcagtttggcggcgg  
 5 cagtgccaaaccaagcagccactgatgaggatacggaaacctcaacattttctctgtggcatcgggacactgtacgaacgtctct  
 aaggatcatgatggttctgctgctaaagcacacaaaatcacctgtgaagttctggttctgaagaactatcttccgccaattacgg  
 atttcttctcacatggccagtgagtacaactccagtacgaattggtccagtacaaatggccccgctggctgcatcagcaaacgg  
 aaaaacagaggaccatttggggctacaagatcctttctggcagctgcttcccgtgaatgtgaggaaaatcatttctggtgatgc  
 cgatgccatcgtaagaacggatataaaggagttgtatgacatggacctcggaggagcacctatgcctacacgccattctgcgatt  
 10 cccgcaaagagatggagggttccgattctggaagcagggatactggcgaagccatctgatgggcaggcgttaccacatttccg  
 cctgtacgtggtggacttgaagagattccgcaagattgcggcaggagataggctaagaggccaataaccaggcacttagccagg  
 atccgaacagcttatcaatttggatcaggacttggccaacaacatgatccaccaggtcgccatcaaatccctgcccagcactgg  
 ctatggtgccaaacgtggtgcagcgacagcaactcaagactgctaaagtattgattgtgcaacaaccgcagaccaaggagg  
 ccaaaactcacggcccccagaggattgtcccgaatggaaggactacgatccgagctgaagaccctgatgtctgcacgcag  
 15 gatcatgagaattcgcatagcagggactcggcagttgatgattcgggtgacgattcgggtgaggtcaccactgtgacgccttctcat  
 gagcccaagcacggcgagctgtga

**Drosophila Gene Hit** rescue sequence and BLASTX with EST and TBLASTN with  
 ORF2: UDP-glucose:glycoprotein glucosyltransferase (U20554)  
 20 **Human Homologue** BLASTX with UDP-GGT: hypothetical protein (AL133051)  
**Drosophila EST** several including GH16576 (AI293351)

25 **Annotated Drosophila genome genomic segment** AE003519  
**Annotated Drosophila genome Complete gene candidate** ugtUDP-glucose-glycoprotein  
 glucosyltransferase

30 **Human homologue of Complete gene candidate** CG6850-  
 IGI\_M1\_ctg14521\_41  
 D65BCE6EEC187AE3  
 TRANS:SEPT20T.ctg14521.2  
 2 FPC\_ctg:ctg14521  
 FPC\_start:1284609  
 FPC\_end:1284696  
 35 FPC\_strand:+ ( 1.20E-215)

**Putative function** ugtUDP-glucose-glycoprotein glucosyltransferase  
 40 **Confirmation by RNAi** Only wild type profiles observed

**Example 26 (Category 3)**

5	<b>Line ID</b> <b>Category</b> <b>Reversion</b> <b>Map Position</b>	430/5 Mitotic defects in brain: metaphase arrest (overcondensation, polyploidy, metaphase with bipolar spindle) NR 98B5-8
10	<b>Rescue ID</b> <b>Rescue Sequence</b>	2C2E GTGCGGCCCATGGATGTGCGAACGTGTACGAAGACCAAGATCGGCATCGCCA TCGGCGGCAGCACGACGGACGATAACGAAAAAGCTACAGCCGCCGCCACAGA TACAGATGCAGATGCCATGCCGCTGTTATCAGCGCGAGCGGGAGAATGATAA GGGATGGGATCGCTCAGCGCGGCAGGCAAGACGACCAAAAAGAGAGCCAAC TAAATGATGTGCCTAAGACTAAGAGTTTAAATGAGCATTACTGTGCGCACTCT ATGTATTATGAATAAAATTCATACAACCTTTGTGGTTTATTATAATAAAAAGT GTGTCAGCTCTACTCGGGGGAAAGTAAGTTTACTTCTTGGCCGCTGGCTTCTTG GCGGCGACCTTCTTCTTGC GGCGGCCAGCAACTTGGCGCGATTGGCGCAGCC TTGGTGGCCACATTGGCGAAGTGCGACTTGGCCAGCTCGACGTTCTGCTTCTT GGCTTGGCCAGCACCTTGGCCACGGTGCGCTTCTCGGCGGCGAGGGCGGCAC GACGCTTGAGTACCTCGGCATAAGGGTTCAACTTGATCAACTTGCGCACGGTT GGTAAGGGGGTT
25	<b>Drosophila EST</b>	several including LD45359 (AI513164)
30	<b>Annotated <i>Drosophila</i> genome genomic segment</b> <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	AE003763 CG5502 RpL1 - Ribosomal protein L1
35	<b>Human homologue of Complete gene candidate</b>	1e-126 432359 dbj BAA04887  (D23660) ribosomal protein [Homo sapiens]
40	<b>Putative function</b>	structural protein of ribosome involved in protein biosynthesis
40	<b>Confirmation by RNAi</b>	Marked decrease in G1 and G2/M indicating fewer cycling cells

**Example 27 (Category 3)**

**Line ID** 472/12  
**Category** Mitotic defects in brain: metaphase arrest. Meiotic defects in testis: segregation defects. Abnormal spindles  
 5 (mitotic: High mitotic index, meiotic: Ab-08/24)  
**Reversion** R?  
**Map Position** 96C7-9

**Rescue ID** 2B6E

10 **Rescue Sequence 1**

GTCTGACGTTCTCTGAGGGCAAAAAGTTTCGAGTTAGTTGAAGGTGAGGGTGCT  
 CGATCACCGATTTGCGGTGAGACGAAAAGAAAAGTATGCATTGTTGCGTTGTAA  
 AGAGAGCCGGCGCTCGTCTTGTTTCACATTGTCGCTGAGAACGTATGTTGTGCT  
 15 TCATCATTTTCCTTGTTGATTTCCCTTTGACGTGGCAACTTGACCATGTATGACA  
 ACTCTTTGGTGGTGCCATCTGGAAGGCAGAAATTTGATGTCAACGGTGCTCCC  
 AGCCAGTCCACTCCCCAACTCACCTGCAGCTCCACTTCGATATTAACGCGCA  
 ACATATTAGTGGCGTAGTTGTACCTGCCGCGGATCCCATTTCCGCTTTGAAAT  
 TTCGCACTTTCGAATATCCGTCCACATTCGATTTGAGAACATCTTCGAAACGTT  
 CAGCGGTGACCCAAATCGGGTATTTTGCCAGCCGCCATTGTAGATAATCGGGAT  
 20 AAGTATTTTGAAATCGAGCAGAAAACACATATACGTCCAGTGTGACGGTCTTG  
 CGTAGACTGATGAAAGCCGAGTATTAGACTCTACACATCTGTGGAGCTTTTAA  
 ATTTCGTAGTGCGCGGCCGATTTCTCTCGATCTTCTCTCAAAAGCTCCGCTAAT

**Annotated *Drosophila* genome genomic segment** AE003751

25 **Annotated *Drosophila* genome Complete gene candidate** CG10618 - novel

**Human homologue of Complete gene candidate** none

**Putative function** no homologies which indicate function

30

**Confirmation by RNAi** Only wild type profiles observed

**Example 28 (Category 3)**

	<b>Line ID</b>	571/15
	<b>Category</b>	Mitotic defects in brain: metaphase arrest (overcondensation, few anaphases, some polyploids)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	93D
	<b>Rescue ID</b>	2A8E
10	<b>Rescue Sequence</b>	GGCGGCGCTACATTTGTTGTTGTCGCTGCTGCTCACAGCTCCACCACCATTTCG ACAGTTATATTACCTCGCTCAAGTCGCCCCCTCTCCCTCTCGCCCACTCGCTGTG TCAATCGAATTAACGAATGCTCTTCGGCGAATAATTGGGTTTAGATACTTT TCCAGCAGACAAAGTTGTATTTTTGCACTTCTTATTGATATTAGGCAAAACGC 15 ATCGGCCGAATCACACGCACACAAAGCACACACGCGAGCAGCGGTTTTTCAA TCTGCAGTACACCAAACAACACACACTATTTCTAATGCCTGTTCTTATCCCTC TGATATTCCCAATGAATCGCTGGGCAATTGGCGATTCTGAACCGATTTTCACTT GGCTCTTTGTTTTATTTAATTTTACCGAAACGCTCTCACACGCAGAGACGCTT TTGCTCGTTGCTGATGCTTCTGCTGCAATACACACCACCTACGAAACGAGCC 20 AAGGGAAATTGTATCTATGGGCTGTGTATCTGTTTCTACGCGGCACGCGCTGC ACGTCCGCTCGCTTCGGGTTTTCGAGAGAGAATAACTTTTTCGATACGGTA CGGTAAACGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCGTGATA CGCCTATTTTATAGGGTAATGCATGATAATAATGGGTTCTTAGACGTCA
25	<b>Drosophila EST</b>	LP07504 (AI294185), LP06548 (AI293427)
	<b>Annotated Drosophila genome genomic segment</b>	AE003734
	<b>Annotated Drosophila genome Complete gene candidate</b>	CG15802 – novel homology to Doom, a product of the Drosophila mod(mdg4) gene, induces apoptosis and binds to baculovirus inhibitor-of- apoptosis proteins
30		
35	<b>Human homologue of Complete gene candidate</b>	none
	<b>Putative function</b>	inducer of apoptosis
	<b>Confirmation by RNAi</b>	Only wild type profiles observed

**Example 29 (Category 3)**

<b>Line ID</b>	736/15
<b>Category</b>	Mitotic defects in brain: prometaphase arrest (overcondensation, fewer anaphases, metaphase with bipolar
5	spindle)
<b>Reversion</b>	NR
<b>Map Position</b>	73C
<b>Rescue ID</b>	H5E
10	<b>Rescue Sequence</b>
15	CTAATGAGTAAGGAAAACCAATCAGCCTTGCTAATCGCTTGGCAGTATTGGCT TCTATGCAGGGGGGGCGTGTCCCGCGCCCCTTGAAGCTCAAATTTTGTCAAGGG CACAGGTCGTCCCTCCTCCTCCGCGTGGGTGGCGTTCGGCCGAACGAACCGG CGCCTACTTTGCGTCCGGCTAGCGAGGATCTCTGGGTGCCACCCACGGCTGG GTGTTGCGATCTGCCCATTGATAATCCATGCGTGAGAAAGCTTTAGAGAATC TGCCAGATTATTACTCCCCGCATACTCAGAAAAATGTATCCTTCAGATATG TTTATGTTTATGAAGTGAAAAAAGTCCTTTGAAATACTACAAAAAGTGAGGAT CTGACCAATGATTTGATTTCTATAGAAATATACTATAAACTATAAACTAC
20	<b>Genomic hit, Accession No.</b> CSC:AC014181
<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003526
25	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b> CG3971 baldspot - with homology to membrane glycoprotein
30	<b>Human homologue of Complete gene candidate</b> CG3791-9e-08 4680391emb CAB41293.1  (AL034374) dJ483K16.1 (novel protein) [Homo sapiens]
35	<b>Putative function</b> membrane protein, function unknown
<b>Confirmation by RNAi</b>	Slight reduction of G1 and G2/M peaks indicating fewer cycling cells

**Example 30 (Category 3)**

5	<b>Line ID</b> <b>Category</b>	82/24 Mitotic defects in brain: metaphase arrest (condensation, no polyploidy, no anaphases, metaphase with bipolar spindle)
	<b>Reversion</b> <b>Map Position</b>	NR 100D
10	<b>Rescue ID</b>	2E3E
15	<b>Rescue Sequence</b>	
20	GGTCAAGCCCGATGGCGTCCAGCGCGGGCTCGTCGGCAAGATCATCGAGCGC TTCGAGCAGAAGGGCTTCAAGCTGGTCGCCCTGAAGTTCACCTGGGTAAGCGG ATAATTGAATTAGGAAGAAATCAATAGATATACATACGTGGAAACGGGTTC CCACGCGGGGTTGCTATCGGACCTAACCTCAAAGGCTGGGTGCAGGCGTCAT CGCGGAATGACATGTGTTTAGAGGTCAGAACTGCAATTAAGTATAACGAACC GTTTTGTAACCAGGCCTCCAAGGAGCTGCTGGAGAAGCACTACGCTGATCTGT CCGCCCCGCCCTTCTTCCCCGGACTCGTGAACCTACATGAACCTCCGGCCCCGTG GTGCCCATGGTGTGGGAGGGTCTGAATGTGGTCAAGACCGGTCGCCAGATGCT CGGCGCCACCAACCCCGCCGACTCGCTGCCCCGGCACCATCCGCGGTGACTTCT GCATTGAGGTCGGACGCAACATCATCCACGGCTCCGATGCCGTCGAGTCTGCC GAGAAGGAGATCGCCTGTGTTCAACGAAAAGGAGCTGGTCACCTGGACCCC GG	
25	<b>Genomic hit, Accession No.</b> CSC:AC012727	
30	<b>Associated ORF</b>	
	Genscan ORF1 predicted sequences >16:43:49 GENSCAN_predicted_peptide_7 172_aa MKLLMLGTLAFFSVISATMAANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLV ALKFTWASKELLEKHYADLSARPPFPLVNYMNSGPVVPMPVWEGLNVVKTGRQ MLGATNPADSLPGTIRGDFCIQVGRNIIHGSDAVESAKEKIALWFNEKELVTWTPA AKDWIYE	
35	>16:43:49 GENSCAN_predicted_CDS_7 519_bp	
40	atgaagctcctgatgctcggcacaattttggcattctttctgtaatctcggcgacaatggcggctaacaaggagaggactttcatcat ggtaagcccgatggcgctccagcgcggtcgtcggcaagatcatcgagcgcttcgagcagaagggttcaagctggtcgcc tgaagttcacctgggcctccaaggagctgctggagaagcactacgctgatctgtccgccgcccccttctccccggactcgtgaa ctacatgaactccggccccgtggtgccatggtgtgggaggggtctgaatgtggtaagaccggctgccagatgctcggcgccac caaccccgccgactcgtgccccggcaccatccgcggtgacttctgcattcaggtcggacgcaacatcatccacggctccgatgc cgctcagctcgtccgagaaggagatcgccctgtggttcaacgaaaaggagctggtcacctggaccccgccgccaaggactgg atctacgaatag	
45	<b>Drosophila Gene Hit</b> <b>Human Homologue</b>	rescue sequence and TBLA; abnormal wing disc (awd) (X13107) BLASTX with awd and TBLASTN with ORF1: tumor metastasis inhibitor nm23-H2 (A49798) non-metastatic cells 2, protein (NM23B) (P22392) and nucleoside diphosphate kinase B.

***Drosophila* EST** several including LP05977 ( AI257573 similar by TBLASTX to X92956 B.taurus mRNA for nucleoside diphosphate kinase (NBR-A)

5 **Annotated *Drosophila* genome genomic segment** AE003779  
**Annotated *Drosophila* genome Complete gene candidate** CG2210 - awd abnormal wing discs nucleoside diphosphate kinase

10 **Human homologue of Complete gene candidate** gi4505409  
1A5C3F84D7AD272C  
|ref|NP\_002503.1| non-metastatic cells 2, protein (NM23B) expressed in [Homo sapiens] (1.90E-61)

15

**Putative function** human nucleoside diphosphate kinase, transcriptional regulation of c-myc expression.a candidate suppressor of tumor metastasis

20 **Confirmation by RNAi** Only wild type profiles observed

**CATEGORY 4: ANAPHASE DEFECT****Example 31 (Category 4)**

5	<b>Line ID</b> <b>Category</b>	1132/8 Mitotic defects in brain: anaphase defects (overcondensation, high polyploidy, some lagging chromosomes)
	<b>Reversion</b>	?
	<b>Map Position</b>	86F3-6
10	<b>Rescue ID</b>	2C3E
15	<b>Rescue Sequence</b>	GGCCGGAGGTACCATTTTGGTAGGACCGTTTTTCGGGCCAACGAAAATACCAC AAGACGGCAGCGATAATAGTGTTTTTGGCTTCAAATGTAGTATGGCTACGCAA CTCACATATGGTTAAGAACTTCGCTGTTTATTTGGTGGTTAACTAGCTAAATA CAATAAGAGTGGCAACGCCGTCACGTTTTCTACATGTATTTTACTTGGCGTAGT GCGCCAAGCTTATAAACCACAGTTGGGCGGTTCTTTTGAATTGTTTAATTTACA CCCCACTATGAACTTATTAGCCTTCTTTATTTATTTTATATTTTATTTTATTTAGGA AGAATACGTTTACTCAAGGTTTCGCAGCTTGTCAATCAGTATTCGCAAATATCA ATAATAAAAGGCATCAATTTTCCAATCAGCAGTTGAAAAGAACTCCCCTCGAC ATTTGAACAAAATGCATTTTTTGGGTGATTATAATTTATTAGAATTTTTTATTGAC TTAAGGTAAATATAAATAAAATATTATTCAAGTACAAAGGTATATATACTCAT TAATANTATTTGGATTCAAGGAAAATATATTTCAAATGGCGGGGGTTTAATA AAACAATTTTTCAAATTAAGG
25	<b>Genomic hit, Accession No.</b>	AC007805
	<b><i>Drosophila</i> EST</b>	several ESTs including LP09688 (AI295922)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003693
30	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG6929 - Lk6 kinase
35	<b>Human homologue of Complete gene candidate</b>	gi4505191 DB39E49EC0BED990 [ref]NP_003675.1  MAP kinase interacting kinase 1 [Homo sapiens] (6.20E-113) and gi9994197 551A82FA3D09FD58 [ref]NP_060042.1  G protein- coupled receptor kinase 7 [Homo sapiens] (1.70E-106)
40	<b>Putative function</b>	Protein kinase associated with microtubules

**Confirmation by RNAi**  
cells

Complete loss of G1 and G2/M indicating fewer cycling

**Line ID** 483/19  
**Category** Meiotic defects in testis: segregation defects  
**Reversion** ?  
**Map Position** 86F

5

**Rescue ID** H2S

**Rescue Sequence 1**

CTCCGGCCACACGGATGAATTCGTCGTCATTCGTCGGAATCATTTCGAACTTTG  
 AAAATGGATCGGTAGCTGGGAAGGAAACTTAAAGCGAAATACGCAAAGAAA  
 10 ACGGCTTTTGTCCGCTATTCAGCGATTTTTTTTTTGTGTTGTAATCAGCAGAGGAA  
 ATTTTAACGACCAACTCCACCGCCACACCAGCCATCTCCAGCAGCCCCGGAAA  
 ATAAAATAGAACTAAATTAACGCCACCATCACTACAACAACCATCTCACCAAC  
 AACTACAAGAGCAACAACCACAGCAACAGCACTACTGCACCAAGCCCACAAA  
 GAAGAGGTGAAACGCAATAATCGA=CAATACCCGAAGAAAAAAACAAAAAA  
 15 ATATCGCAGATAACCGAAAAAAGCGGTGCAATAGATAAACCCCATTTTTTGCT  
 TGAGCTTTTTTCGCCTGTGTGATGAGAGAAATCAGCAGCAGCCATCGATTACA  
 ACAACAACAGCAGCCACACCAACGACGACTCACCACCAAACGAAGAATAATA  
 ACCAGCGGANAGCGATAGATA

20 **Genomic hit, Accession No.** CSC:AC018284  
***Drosophila* EST** several including GH28825 (AI517767), LP04213

Other results same as 1132/8

**Example 32 (Category 4)**

5	<b>Line ID</b> <b>Category</b>	1422/14 Male and female sterile, small wings, meiotic defects in testis: segregation defects, elongation defect
	<b>Reversion</b> <b>Map Position</b>	NR 90B4-8
10	<b>Rescue ID</b>	2F1E
15	<b>Rescue Sequence</b>	GGCCAGCTGCTCAAACATTCTGCAGCTATTTGGCCGCCAGCGAGTAGAACGAT ATTGCCAAATATTTTATAATAGTAACCAATACGTTACCAGTATGACCGCGCCG ATAACGATAGAAAATACCACACGGTCTAAAAGTAAATACCATTTGGGGTATTC CCTAATCTTTGAATTATTTACCGTTAGGTTTCGGTCGTTTTTTTTTGTGTCAGCTG TTCTTTGTATGAAACGGATTAGTAATTTTATTTGTTGTTTTTGTGCATTTTTGCA TATTAAGCCCTTGAAACATGCCTTAAATCGTTAAAATAGATTATAAGAGGGA TGGACTGTTTGTTAAAACCAATTGGAAAATTTGTAATCGCTGGTAATAACTAT CGAGATAAGCTTAATTATCGCTGTTTTCTTTGTATCTAGTTATAAATAATAATA ATAAACTGGTAATTAACAAAAGTAAAAAGTTACTTAAGTTATACAAAAATAT TTAGTTATTGNATTCAATAATAAGATGGTAATAATAGATGGTAAGATAGTAAT ATTTTAATAATTGAATTTTCATCACACATGCTGGTGCACGTTCCACAACCTACAA TCAAACGAAA
25	<b>Annotated <i>Drosophila</i> genome genomic segment</b> <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	AE003718 CG7623 - novel with homology to UDP-galactose transporter.
30	<b>Human homologue of Complete gene candidate</b>	2136348 UDP-galactose transporter related isozyme 3 - human >gi 1669564 dbj BAA13527  (1e-36)
35	<b>Putative function</b>	sugar modification protein

**Confirmation by RNAi**      **Slightly reduced G2/M**

**Example 33 (Category 4)**

**Line ID** 1479/10  
**Category** Mitotic defects in brain: anaphase defects  
(overcondensation, anaphase bridge, metaphase with swollen  
chromosomes and bipolar spindle)  
**Reversion** NR  
**Map Position** 69F3-7

**Rescue ID** 2D6E

**Rescue Sequence 1**

CCACGGGCAAATGTGGTCCGGAGGTCCACGACAACGTGCCGCTGACCATATC  
CCAGATTGAGCGCGCAACTCAGGATCCGGAGAACGAGAATGTGTTTCATCACA  
GACGACGTGCATCCGATTCACTTCTGCACCTGCATCATCTACGCCTTTGTAAC  
GGCAATGGAACGCACAACGAGTCGTTTCATGAAGTTCATGATCGATGATGGCA  
CCGGCTCCCTGGAGGCCAGCATCACCAAAAAACCCTTCAATGGACGCGTGATC  
AGCAGCCTGTACAGTGAAGCCAGTTCGCTGGCCTCGTCCGAGGCCTACAAGA  
GCATTGCCGTGAGCATGATGCGGCTGCTGCAGGTCTCCATGGAGTACATTGAT  
CCCACGCGCATCTCGAGGGGCCACAGCCTATTCCTGCGCGGTCTGTCGAATAG  
GTTCCGCGGCAAGATGGGTCTGGACGCTTTTCAGTTCTTCATAGACAGCGGCC  
GATCGCGGAATATGGAAATTGGCTTCGTGGACTACCTAACCGACTGGCAACG  
AAGGCATAAAACAATGCAAAATAC

**Rescue ID** 2D6P

**Rescue Sequence 2**

GCCCGTGGACTTTTCACTCTGTTGATTCTTGCGTATCACGAAGTTATCCAGCTG  
GCTTTCTATGTCCTCGAAACTCTGATTAAAAATCCATTCTATTTGCTTAGTCTGC  
GATTTCAAAGGGGATTCTTTATTGCAGTGCATTTTGCATTAGCGCCAAAAAA  
AAAAAAGTTGTGAGCATGGGCGTAGACTTCGTATTTTCTTACAAATAATATTA  
ATTAATAATTAATTTTGTGAGCAATTTTACACAATTGTATTATAAGTTAAACC  
AGGGTCACATTAATTTGCAGAACCGCGCAATATTTTCTTTTAACCCCTTACA  
AATTTTCAGTTGTTTTGACTACGCCCTGCTAATTTTACTTATTAAATTCAAA  
GTCTAAAAACATTGTCACCAGATAATACGAGTATACTATATGGACAAACGT  
AAAATCGTTAATAGAATATATATTTCAACCATTATTTCAACCACCGAGAGAAA  
TTCATTTGCACAAAACGCCAGGTTGGCAGCACCATCATTGCGCACAGCAAGTG  
GGCAAACCTCGTTGTATCGCTTG

**Genomic hit, Accession No.** AC007328

**Associated ORF**

Genscan ORF1 predicted sequences >17:42:01|GENSCAN\_predicted\_peptide\_2|1507\_aa  
MKLAPTVKLNNGYEMPILGLGTYNLKKSRCEAAVCHALEMGYRHHDTAYLYRNE  
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LYLMHSPVGVVDYISDEDLMPHENGQLRTNDVDYVDITYRSMEQLVHLGLVRSLG  
LSNFFNANQLKRLLENCQIKPANLQIECHPELVQVPLIELCKFHNTTVVAYSPLGRSQ  
TCNPLPDYYTDSKLLALAAKYGKTPAQIILRYLSKDNEGEAAVKHAIDVGYRHID  
TAYFYQNEAEVGKAIRDKIAEGVVKREDIFLVTKLWNIFHDPERVEGICRKQLSNF  
GLDYIDLILMHMPVGYKYVDDNTLLPKNEDDVLQLSDVDYLDITYKAMEKLVKL

GLRIEQLAGLSHLSTHSDGMQFRIRMFLTFQRGGPSHNNMQQQQQRGGGSGTDF  
YNQQRDRRDSGRQMDNNYSNNYNNNNNNNNQRNRGGGNGMQQQQRGGNGGSGG  
GGGNGGGNNPAWNMHRGNQNSNNMMNMRNRGMGSRGPMRPNQVHLLVHT  
AIDGLLNPGFHILQGYRPSANNQNKPRNKIKFEGDFDFEQANNKFEELRSQLAKL  
5 KVAEDGAPKPATNATAATATATNEQVGEKVEGVHTLNGETDKKDDSGNETGAG  
EHEPEEDDVAVCYDKTKSFFDNISCEAAQDRSKNKKNDWRQERKLNTEFTGVSS  
TRRGSAVHQLNVFQAVTADATNTTTIMATAALTRDMEERQATTGTIIAWVGGGG  
NFRNRSNNRNNGGGRGNGMPNITNGNTAAALKAANNAAGHGSNATDSSAPNA  
TTATTKSTSLLEPQTQQVAAVSLPVLLPSIGWLFIVMDGPPDIPRSADIAILFVSFEQ  
10 SVLFLKFHKRYNEFAHLLCAMMSFEDIESQLDNFVIRKNQQSEKSTGKCGPEVHD  
NVPLTISQIERATQDPENENVFITDDVHPIHFCTCIYAFVTGNGTHNESFMKFMID  
DGTGSLEASITKKPFNGRVISSLYSEASSLASSEAYKSIAVSMMRLLQVSMEYIDPT  
RISRGHSLFLRGRPNRFRGKMGVCTNATAPSVSSINRILRNRAAERAAEFARAAS  
YGYAIHPHHPYTSFPTWPAHHPLWGAVPLATPPGGGPAGAGGALQPGSGSSY  
15 GSDGNMSSNPSSNSNTTHSNGHNTNSGSGCGDSSAGSGRLSLPALSPDSGSRDS  
RSPDADANRMIDIEGEDSESQSDSQPKFRNRRTTFSPEQLDELEKEFDKSHYPCVN  
TREKLAARTALSEARVQVWFSNRRAKWRRHQRVNLIKQRDSPSTSSSPTPLVNPV  
VSPVSPVPVPVAVPESGQQKQPYPYSTSNMCNTSSSSSNSQPCNTINPGSKMSSK  
TSSVSSNQHMEEPAAVATASPTASAPLSMGGENSAFRALPMTLPMPMTLPTASA  
20 AAFALS FARQYIAKTLLGSPPRSQPPTTNQHKPEPNREFLNEACSSAASVQNSTTP  
ATTADTPTAKSAMCVHCEKKGGAMEWM

>17:42:01|GENSCAN\_predicted\_CDS\_2|4524\_bp

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35 agcgcgttagggcatttgcgcaagcagttaagcaattttggttgactatcgtatctgtatctgatgcatacgccagtggtgcta  
caaatatgtagatgacaacacctgtgccccaaaatgaggacgatgtgctccaactgagcgatgtcgactatctggatactgaca  
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agtctcgatagcggatgttttaacattccaacgtggcggaaccagccacaacaatatgcagcagcagcagcaacgaggcggcg  
gcagtggaaacggacttctataaccagcagcggtgctgctgggactccggacgtcaaatggacaacaactatagcaacaactaca  
40 acaacaataataataatcagcgaatcgcggcgccggaacggaatgcaacagcagcagcgaggaggaaacggcgccagc  
ggcgggcgcggtggaacggaggtggaacaacccggcctggaacatgcatcgcggcaaccagaactcgaacaacatgatg  
aacatgcgcaaccgcggcatgggacccgcggccccatgcgaccaatcaggtacacctgctggtgactcacactgctatagat  
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45 ggtggtgcaccaagccagccaccaatgcaacggcgccactgcaactgcaaccaatgagcaggtgggtgagaaggttgaa  
ggcggtcacacactgaatggcgagaccgacaagaaggatgattctggcaacgagaccggcgctggagagcacgagcctgagg  
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atcaactgaatgtattccaagcagttaccgcggacgcaaccaataactacaacaataatggcaacggcggcattaactcgggatatg  
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 aatgctgctggccacggatccaatgccacggactccagtgccacaaatgccacaaccgcgacgacaaaagtcgacgtccctcttg  
 5 ccagagcagacgcaacaggtggcggcagtttcgtgcccgtgtgttaccatcgattggttggctttttatcgttatggatggaccac  
 cagacattccaagatcggcagatattgcgattctcttcgttagtttgaaacaaagtgtacttttccttaaatcacaagcgatacaacg  
 agtttcccacttgctgtgcgaatgatgagtttcgaggacatagaagccagctggataacttcgtgatacgcaagaatcaacag  
 agtgaagagtcacgggcaaatgtgtccggaggtccacgacaacgtgccgtgaccatatccagattgagcgcgcaactca  
 ggatccggagaacgagaatgtgttcacacagacgacgtgcatccgattcactctgcacctgcatcatctacgccttgaactgg  
 10 caatggaacgcacaacgagtcgttcacgaagttcatgacgatgatggcaccggctccctggaggccagcatcaccaaaaaacc  
 cttaatggacgcgtgatcagcagcctgtacagtgaaagccagttcgtggcctcgtccgaggcctacaagacattgccgtgagc  
 atgatgcggctgctgcaggtctccatggagtacattgatccacgcgcacatctcgagggggccacagcctattcctgcgcggctgc  
 cgaataggttccgcggcaagatgggtgtctgcaccaatgccactgctccttcggtgagcagcatcaatcgcatattcgtaatcga  
 gcgggcggaaggcgagctgcgggaatttgcctggcgggcgagttacggctatgccatccatccacacatccgcatccgtacacc  
 15 agttccccacttggccggcgcatcatccgctgtggggagccgtgcccctggccacgccacctggtggcgccctgctggagcc  
 ggtggtgactgcagccggcgagtgagcagcagctatggcagtgatggcaacatgagctcaaatcccaatagcagcaaca  
 gcaacaccacccacagcaatggccacaataccaacagcggcagtgatgcggggatagtagtgccggaagtggacgcctctc  
 cctgccggcactttcgcggattccggaagtagggacagccgctcccagacgcagatgccaatcgatgatagatatgaagg  
 cgaggacagcagtgccaggaacagtgaccagccgaagtccggcgcaatcgaccaccttcagtcggagcagctggatgag  
 20 ctggagaaggagttcgacaagtgcactatccctgcgtgaatacccgcgagaaactggccgcccgagcggcactgagcagg  
 ccagggtgcaggttttggtttccaacagacgagcgaatggcgggcgccaccagcgggtcaacttgatcaagcagcgcgactcg  
 cctcgcacatcgagctcacccacgcccgttggtcaatccggtgggtcagtcgggtcagtcgaatccagttccagttccagttg  
 ccagaatctggccaacagaagcagccatattcgtagcaccagcaacatgtgcaacaccagcagcagcagcagcaacagtc  
 aaccgtgcaacacatcaatcccgagcagcaaatgagcagcaaaaccagcagcgtcagcagcaaccagcacatggaagagc  
 25 cagcagcggcggtggccactgcctcaccacagcatcagctccattatcaatggcggtgagaacagtgcatcttcgcgtctgcc  
 catgaccttgccgatgccatgaccttgcacagcagcggcgcccttcgcgtcagcttcgcccggcagtcacatagccaa  
 gacgcttctcggttctccagatccagatccagccaccaaccaccaaccagcataagcccagccaaatcgagttcctcaat  
 gaagcctgcagctccgagcatctgtccagaattcgacaacgcggcaacaaccgcagatactctacagccaaatcagcaatg  
 30 tgcgtgactgcgagaaaaaggaggggccatggagtggatgtga

**Drosophila Gene Hit** BLASTN with rescue sequence 2: Histone acetyltransferase GCN5  
 (AF029776) very small match at end, TBLASTN with ORF1:  
 middle domain histone acetyltransferase GCN5 (AF029776).  
 Genomic matches histone acetyltransferase

**Annotated Drosophila genome genomic segment** AE003541  
**Annotated Drosophila genome Complete gene candidate** CG4107 -Pcaf /GCN5 histone  
 acetyl transferase  
 transcriptional activator  
 protein  
**Human homologue of Complete gene candidate** gi6382076  
 72F516F8BD10CD0C  
 [ref]NP\_003875.2| p300/CBP-  
 associated factor [Homo  
 sapiens] (1.20E-197)

**Putative function** Transcriptional activator

**Confirmation in RNAi**

Only wild type profiles observed

**Example 34 (Category 4)**

**Line ID** 184/5  
**Category** Mitotic defects in brain: Anaphase defects.  
 5 (overcondensation, aneuploidy, some lagging chromosomes and breaks)  
**Reversion** R  
**Map Position** 71B

10 **Rescue ID** C4E  
**Rescue Sequence**  
 CTCGAGCAGATGTGGGACGAGCTGAGCGGAGCGCACAAACTGCCAAGTAAGT  
 GGAGCATGTGGATGAAAGGAGTTCCCAGAACAGTGTTGCCAACCAAAAAAAAAA  
 AAAAAAGTTAAAAAGTTAATTTTAATAGTGTAATAAATATGAATTAAATTAA  
 15 ATTTTATGTAAACAGTATTAGCTTTACATGAGATTACCAAATTGTGAGTGTCT  
 GTGTTTGTGTTGCTTTTAAAAAAGTTTAAAAAGCACATAAAGAAATATATTTTAAA  
 TTTAATTAAAAAGTTTCGTAAAAAGTAAAAAGGTAGCTAAATTAAGTTTCCT  
 ATTCAAATCAGATTTGGCGAACAAAGAGCCAAGTTGGCAACACTGACAATGA  
 CTCCAAGCGCGAACAAAGCGATTTCTATCGTTATCCCACTCTCTCTCCAGAG  
 20 ATCGTTCTCAAGGCCAAATGGAAGGGACTTCGAGACAATTTCCGTGTGGAGTC  
 AAAAGGATCCGGCGGCCGAATAACGG

**Genomic hit, Accession No.** CSC:AC019852

25 **Associated ORF**  
 Genscan ORF1 predicted sequences >22:43:26|GENSCAN\_predicted\_peptide\_2|1003\_aa  
 MAPKKSTIVLNVEQFIHDIEERPAINRNFHCNKAFLQMWDELSGAHKLPKIVL  
 KAKWKGLRDNFRVEYKRIPRADNGDFMVDPATFESKWLHYYALLFLTDMHRHR  
 LPKNEQDQSFYFSQQSEDCEKTVVEPDLTNGLIRRLQDSEDEYDEEEMEADGEAS  
 30 EATMEETMPTPPAAHQMNQVSTTPLATGALRAQEEAHQHALIKAGLLRAQLMEL  
 EKEAEDLSRKPPPPQMTSPVAPSLQVLVEPPAAHCSPPPMVTTTSAQVQQPGSA  
 AVLAPATTTSSASSVSSNGAPMGGKRSVSPPPLYNKAHHPLATLAAHLAAKDRN  
 EDFGPTSAVGGNGDHLSTQHSYANGLIPALKLKRPRLSNDFNGSSTMDTLPVP  
 EDDDYHYLLSLHPYMKQLTAAQKLRIKTIQKLIFKELYKEDLEESNLDREVYVL  
 35 DDGAEVDLDLGNRYERFLDVTLHRDNNITGKIYKLVIEKERTGEYLGKTVQVVP  
 ITDAIQEWVERVAQTPVQGSKPQVCIVELGGTIGDIEGMPFVEAFRQFQFRVKRE  
 NFCLAHVSLVPLPKATGEPKTKPTQSSVRELRGCGLSPLIVCRSEKPIGLEVKELI  
 SNFCHVGPDPVICIHDLSIYHVPLLEQNGVIEYLNERLQLNIDMSKRTKCLQQ  
 WRDLARRTETVRREVCIAVVGKYTKFTDSYASVVKALQHAALAVNRKLELVFIE  
 40 SCLEEEETLHSEPSKYHKEWQKLCDSHGILVPGGFGSRGMGKIRACQWARENQ  
 KPLLIGICLGLQAAVIEFARNKLGLKDANTTEIDPNTANALVIDMPEHHTGQLGGT  
 MRLGKRITVFSDGPSVIRQLYGNPKSVQERHRHRYEVNPKYVHLLLEEQGMRFVG  
 TDVDKTRMEIIELSGHPYFVATQYHPEYLSRPLKPSPPFLGLILASVDRLNQYIQRG  
 CRLSPRQLSDASSDEEDSVVGLAGATKSLSSKIPITPTNGISKSCNGSISTSDSEGA  
 45 CGGVDPTNGHK

>22:43:26|GENSCAN\_predicted\_CDS\_2|3012\_bp

atggcgccaaaaaagtcaccattgtgctcaatgtggagcagttattcacgacatcgaggagcgccggccatctggaaccgca  
 atttccactgcaacaaggccttcctcgagcagatgtgggacgagctgagcggagcgacaaaactgccaaagatcgtgctcaagg  
 ccaaatggaagggaacttcgagacaatttcggtgtggagtacaaaaggatacccgggcggaataacgggtgattttatggtggatcc  
 5 gggccacctttgagtcgaagtggctgcactactatgcattgttgttttaactgatcacatgcgtcatcgtttgcaaagaacgaacagg  
 atcagtcattttacttcagccagcaaaagcgaggactgtgaaagacagtggtggagccggatttaacaaacggctcaatacgtcgt  
 ctgcaggacagcgacgaggattacgacgaggaggaaatggagggcgacggagaggctagcgaagccaccatggaggaaac  
 gatgccacgccaccggctgcgcatcaaatgaatcaagttagcaccacaccactggccaccggagctttgcgagcccaagaag  
 aggcacatcagcacgctttaattaaggcaggattactccgcgctcagttgatggagctggaaaaggaggcggaggacttgagca  
 10 gaaagccacctccgccacagcaaatgacatctccagtggcaccctcactacaagtgtagtggaaaccaccagccgcacactgtt  
 ctccaccgccaatggtagaccaccacatccgcacaagtacaacaaccgggctcagcagctgttctggcgccggcaacgaccaca  
 tccgctcatctgtatcctcgaatggagcgccaatggcgcggaagagatctgtgtcgcaccgcctctatacaacaagcacacc  
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 acggagatcacctgagcttcaactcaactcctacgccaatggactgataccggccttaagctgaagcgcccgctctctccga  
 15 ggtatgcaatttaattggttcctcgacaatggacactccgctcgtaccagaggacgatgactaccactacttgcagcctacatcc  
 gtacatgaagcagctgaccgcagcccagaagctgcgcatacgcaccaagatacaaaaagctcatcttcaaggaaacttacaaga  
 agatcttgaggagtgcaacctagatcgaggtttacgttttgacgatggcgccgaggtggatctgggaaactatgaac  
 gggttttgatgttaccctgcacgggacaacaataaccaccggaaaaattacaagttggtcattgagaaggagcgactggc  
 gactactgggcaaaacggttcaagttgtcccacacatcactgatccattcaggaatgggtggagcgcggtggccagacacc  
 20 gttagggatcttcaaagccacaggtgtgcatcgtggaattgggaggaacgattggtgacatgaaggcatgcctttcgtagagg  
 ccttcgctcagtttcagttccgcgtaaagagagagaactctgtttggccatgtgtcgtggttccgttgccaaaggctaccggag  
 aaccaagaccaagcccacacaagttcgggtcagagaactgagaggatgtggcctgagtcgccgatttgattgtctgccgatcggg  
 gaaacccattggactggagggtcaaggagaagatcagcaacttttgcattgtggggccggatcaggtgatatgcaccacgatttga  
 actccatttatcatgttccgctgctgatggagcagaatgggtgtattgaatacctaataatgagcgctacagcttaatacgcacatgagc  
 25 aagaggaccaaatgctgcagcaatggcgagatttggcgctgcaacggagaccgttcgccgtgaagtttgatcgcgcgtcgtg  
 ggaaagtacaccaagttcacggattcgtacgctccgtagttaaagccctgcaacatgccgcctggcagtgaaatcgcaaaactgg  
 aactggtctttatcgatcgtgctcgtggaggaggaaactttgcattctgagccgagcaagtagcacaaggagtggcagaagct  
 atgcgatagccatggcatcctagtcctgggtgattcgttccgtggaatggagggaagattcgtgcatgcaatgggcgcga  
 gagaatcaaaagccattgcttggcatctgcttgggtctgcaagcgcggtcattgaattgcacgaaataaacttggctcaaggat  
 30 gcaaacaccacagaaatcgatccgaacacagctaattgccttggctatcgatatgccagagcatcacacgggtcaattggcgggc  
 actatgcgcttgggcaagcgaataactgtttctctgatgtgctcattgcagttgtatggcaatccgaaaagcgtgcagg  
 agcgtcatcggcatcgttacgaggttaatccaaatcgtgcatctgctggaagagcaaggcatgcgatttggggcaccgacgt  
 cgacaaaactaggatggaaatcattgagctcagcggctacccctacttgttgccaccaatcatccagagtactgtcgcggcc  
 tctgaagccgtcgcctcttctcctggcctgacccctcagtgatcattgaaccaatataatcagcgcgggttgcgcgctgtc  
 35 ccccgccagctatccgacgcatcctcgatgaggaggacagtggtgtgggttggccggagcaacaaaatcgtgagctccttg  
 aaaatccattacaccacaaaatggaatatcaaaaagttgcaatggtagcataagcacttccgacagcgaaggtgcctgcggag  
 cggtgacatccaatggccataagtaa

**Human Homologue** TBLASTN with ORF1: CTP synthase (CTPS) (NM\_001905.1)

40 **Drosophila EST** LD27370 (AA941993)

**Annotated Drosophila genome genomic segment**

AE003532

**Annotated Drosophila genome Complete gene candidate** CG6854 - novel protein,  
 possible CTP synthase?

45

**Human homologue of Complete gene candidate**

gi4503133

C33BD849A0044697

|ref|NP\_001896.1| CTP

synthase; cytidine 5-prime  
triphosphate synthetase  
[Homo sapiens] (8.40E-217)

5

**Putative function**      Enzyme important in the biosynthesis of phospholipids and  
nucleic acids, and plays a key role in cell growth, development,  
and  
tumorigenesis. The region of the human gene is the location of  
breakpoints involved in several tumor types

10

**Confirmation by RNAi**      Loss of G1 and G2/M peaks indicating fewer cycling cells

**Example 35 (Category 4)**

- 5    **Line ID**                    225/27  
      **Category**                Meiotic defects in testis: segregation defects  
      **Reversion**                NR  
      **Map Position**            90D
- 10   **Rescue ID**                2D2P  
      **Rescue Sequence 1**
- Rescue ID**                2D2E
- 15   **Rescue Sequence 2**  
      GCCTGAACTTAAAACGCTGCCTTCGGCTCTCGCTCGGCACTCGCTCGGCTGCG  
      ACGTCGACTGCGACGCTGGCAGCGACAACAACGATTGGCCTCTCTCATTCACT  
      TACCTCCTCTCTCTCTCTCGCACTCTCTCTTAGCGGTGAGAGAGTGTTTTCTC  
      ACATTTGTTTTGCTTTTTCGGTTCGCCAATGGCCCCCAAAACGAAAAGAGCG  
      20   CGCAAGAGCTAGCTCCACAGTGGATCCTAAGAGAACGGTCCCTGTGGACTCC  
      ATCTAGCTAAGAGAAACGCACTTAGTTAGTTTCTATTTTTGGTTGTTAAGTAC  
      TGCTAGCTGCCTGCCAGTTGAGTGTCCGTCCAAAACGGTGGTGGAAATGGGG  
      GTGACCACTTCAAACATGAAAGCGAAATGTCCTGAGACCCTACAAAACTAG  
      AAATACGCGGGTGCCTGAGAGAAATTTTTTATTTCAAGTAAATTGGCAGAGG  
      25   CTACATTTTGAATGTTTCACAATGAAAATTGCTGGGGAAGCTAGTGAACAACCA  
      TTTCGCCATAATTACACTATCTAAGCTTTTATTTTATAGCCACATGATATATGC  
      ATGCA
- 30   **Genomic hit, Accession No.** AC008361
- Associated ORF**  
      Genscan ORF1 predicted sequences >20:36:39|GENSCAN\_predicted\_peptide\_2|515\_aa  
      MSSTIRLQTSSCQCCKLYKYERHPNKP NLQPTPIP NYPCEILHIDIFALEKRLYLSCI  
      35   DKFSKFAKLFHLQSKASVHLRETLVEALHYFTAPKVLVSDNERGLLCPTVLNYLR  
      SLDIDLYYAPTQKSEVNGQVERFHSTFLEIYRCLKDELPTFKPVELVHIAVDRYNT  
      SVHSVTNRKPADVFFDRSSRVNYQGLTDFRRQTLEDIKGLIEYKQIRGNMARNKN  
      RDEPKSYGPGDEVFVANKQIKTEKARFRCEKVQEDNKKNRNGKAAGGKGKTR  
      RVARGAQIYQNWAICRNLF LFLSLACCRVCKVCDIVVEFRKGTNAVNVQIREAI  
      40   SHVFHKEDIVIDVQESKEWCIWTDQVQSPLPELENLWHELWIGPSHAYLIDQIVD  
      LFENLLEKYNVQVVDVVRFNFLHRA LVVVIISGIIIIIIIMIGVSGGQRTNAFHHRS  
      QRSAIGGDPQQKDSAVQQVQARSSDAFCQIPHRSPRFPGRSQLIPKPNREILRNASA  
      TKNLLFRIRSQ
- 45   >20:36:39|GENSCAN\_predicted\_CDS\_2|1548\_bp  
      atgtccagtacgatccgtctgcaaaactcctcatgtcagtggtgcaaaactctacaagtacgagagacaccctaacaaccaaaccta

caacctacgccaattcctaactacccatgtgaaatacttcacatcgacattttgcgctcgaaaaaggttatacctaagttgtattgac  
 aaatttagcaagtttgccaaactttccatctgcagtcaaaagcatctgtgcatttgcgagaaactttggtggaggccctacattacttc  
 accgcccctaaggtcttggttcggataacgagcgagggttggtatgccccacagtgtcctaactatcttcggtctctagatatcgatct  
 gtattatgctccaaccagaagagcggaagtaaatggtcaagtcgagagattccactctacgttcctagaaattatcggtgcctfaaa  
 5 gatgagctccctacctcaaacccgttgagctggtacacatagcagtgaggcgtacaacacttcggtcactcggtaacgaatcg  
 aaaaccagcagacgttttttcgaccgtcgtcaagggttaaatatcagggtctgacagatttcggcgccgagactttagaggacat  
 caagggttaattgagtataagcaaattagaggtaatatggctcggataaaaaatagggacgagccaaagtcttatgggcccggga  
 gatgaagttttgtgcaaataagcaaataaaaaaaaaggaaaaagcgaggttcagatcgaaaaaggtacaggaagacaacaag  
 aaaaatcgcaacggaaaagcgggggtggaaaggggaaaaactcgagagtagcccgtggagctcagatttatcaaaactggg  
 10 caatctgccggaatctgtttctgtttctgtctcttgcctgctgccgagtggtgtaaaagtgtgtgatatagtcgtagaattcagaaaaggaa  
 ccaacgccgtcgtgaacgtgcagatccgtgaagctatcagccatgtgttcataaagaagacatagtcgatcgcaggaggtcc  
 aaggaaatggtgtatttgaccgatgatcaggtgcagtcgcctctgccagaacttgagaatctgtggcatgaactgtggataggccc  
 tagccatgcgtacctgatcagatcagattgtcgatctctcgaataatctgctcgaaaaatataatgtgcaggttgctgatgtagttcgggt  
 caatttctccatcgcgctctcgtagtcgtgatcattcgggtatcatcatcattatcatcatgatcatcgccggttagcggcgccca  
 15 aagaacaaatgcctttcacaccaccgatctcagcgatcagcgatcgccggcgaccctcaacaaaaagattcagcggtgcaaca  
 ggtgcaggcacgatcttcggatgccttttgcagataccccaccgatctcccagggtcccaggcgccagccaacttattccgaagc  
 caaatcgagaaattcttcgaaacgcgagtgccacaaaaattattgttcgaattcgcagccagtga

20 ***Drosophila* Gene Hit** BLASTN with rescue sequence: couch potato (Z14974).  
**Human Homologue** BLASTX with couch potato: RBP-MS/type 2 (RNA binding motif family)(D84108)

25 **Annotated *Drosophila* genome genomic segment** AE003720  
**Annotated *Drosophila* genome Complete gene candidate** CG18434 -couch potato RNA binding protein  
 30 **Human homologue of Complete gene candidate** 2224621 dbj|BAA20798|  
 (AB002338) KIAA0340  
 [Homo sapiens] (2e-19) and  
 Ensembl predicted peptide  
 Gene:ENSG00000070877  
 Clone:AC009710  
 35 Contig:AC009710.00004  
 (predicted unknown protein)

**Putative function** Possible RNA binding protein

**Example 36 (Category 4)**

**Line ID** 238/37  
**Category** Meiotic defects in testis: segregation defects, multi-stage defects  
 5 **Reversion** ?  
**Map Position** 70D

**Rescue ID** I7E

10 **Rescue Sequence**

GTTCAAACGCACTTTTAAGGTGGCCTATCGGCCCATCAGGAGCAACTTTGTTC  
 TGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGG  
 TCTTCGCTCCATTAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTCT  
 GATTAGGACACGGGCTGCCTGAGCTTGCAGTACAATGGTCGGACGCACTACG  
 15 CCTCCTGGGCGCCACAAAAGGGCGGCGGCATTAAAGACACCGAGATTGG  
 GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCGG  
 ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATCTGCCCCG  
 TACCTCGTACGCTAGCAGCACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGA  
 GAATGATCTGGTCAAGTGTGCGCTCATCGCTGACGTTCTCAACCTGCGCAGCG  
 20 TCCACGTTACCCCCGTCTCGTCCAAGGACTGGGAGATCATAGTGAGTGACGGT  
 TTCGCCTGCTTGGCGGCGTGG

**Genomic hit, Accession No.** CSC:AC017664

25 **Associated ORF**

Genscan ORF1 predicted sequences >15:26:30|GENSCAN\_predicted\_peptide\_1|1819\_aa  
 EMVQAKDPPSHYLSKLRTYLDPKASRSHRLYLFYFLCQKRKMVGESTSTQVLRD  
 LEISLRTNHIEWVKEFLDDTNQGLDALVDYLSFRLQMMRHEQRLQGVLCASEERL  
 NLTNGGDGGEIVMGNSSSVSPGGGGGLLSHGNSTGHGLANGTLDSRQQHTMSYG  
 30 FLRPTIADALDSPSLKRRSRHIAKLNMGAAATDDIHVSIMCLRAIMNNKYGFNMVIQ  
 HREAINCIALSLIHKSLRTKALVLELLAAICLVKGGHEIILGSFDNFKDVCQEKRRF  
 QTLMEYFMNFEAFNIDFMVACMQFMNIVVHVEDMNYRVHLQYEFTALGLDKY  
 LERIRLTESEELKVQISAYLDNVFDVAALMEDSETKTSALERVQELEDQLEREIDR  
 NSEFLYKYAELESESLTLKTEREQLAMIRQKLEELTVMQRMQLQHNEQELKKRDT  
 35 LLHTKNMELQTLRSLPRSASSGDGSLANGGLMAGSTSGAASLTLPMPMPASP  
 TASSAAPPPPPPPAPPAPPPPPGFSPLGSPSGSLASTAPSPPHAPPMMLSSFQPPPPPPVA  
 GFMPAPDGAMTIKRKVPTKYKLPTLNWIALKPNQVRGTIFNELDDEKIFKQIDFNE  
 FEERFKIGIGGALRNGSNGTEVDGSLQSSKRFKRPDNLLEHTRLRNIAISRRLG  
 MPIDDVIAAIHSLDLKKLSLENVELLQKMVPTDAEVKSYKEYIIRKQDQQLTEED  
 40 KFMLQLSRVERISSKLAIMNYMGNFVDSVHLISPQVQSIAGASTSLKQSRKFAVL  
 EIVLAFGNLYNSNKRGPAYGFKLQSLDTLIDTKSTDKRSSLHYIVATIRAKFPELL  
 NFESELYGTDKAASVALENNVADVQELEKGM DLVRKEAELRVKGAQTHILRDFL  
 NNSDKLKKIKSDLRHAQEAFFKECVEYFGDSSRNADAAFFALIVRFTAFKQHD  
 QENEQRLRLEKAAALAASKKENDQVLMRNKVNQKKQAEAVINELKSKAHSVRE  
 45 KKLLQQDEVYNGALEDILLGLKSEPYRRADAVRRSQRRRIDNNRLSRTLEEMDCL  
 HENDLVKCALIADVNLRSVHVTPVSSKDWEIIEELSTEKISGSVLEQTRIVNSTQILI

VWINKSMQVALTVDRCLKPHMNYGRIDHNTELVVAPNLYKGLTNGTSNGVIEENT  
 KLSRSKTTAQVKDELTEKLTPLTHSSTVSNVKNITQNRKRQDHMERLKKDLRRES  
 SRSFEFRVIRGLWREQAQESDVFNKGHLPEFFDLDFYCMHTAADKDYYVRVR  
 TVEDDIEDDLPETIHPSIELNANLMKLLGIKELERVVLRPKTTVVNFVEKIELFANK  
 5 KTHYKIMENAFKRFVIERTQHKPMLFNQEEVVRLEDDLLVTVGILPEHFRYCVVD  
 AQFLKESKIYAADLVRPVGEIKEETPPTSPLSVQDLIQLPEYDKIVDQVVQELRMN  
 LCLSADNSVMRQCNVLLAGASGTGKTVLVERILDQLSRKPDYCHFEFFHGSRSKG  
 RKTESIQKDLRNIFTSCLQHAPAIVVLENLDVLAHAAGEQSSQDGEYYNRMADTV  
 YQLIVQYTTNNAIAVIATVNELQTLNKRLLSSPRGRHVFTVARLPNLERADREILR  
 10 ELCSHINVAKDLDLVKFSNLTEGYRKCDLVQFVERAIFYAYRISKQTPLLNDQLI  
 ESLEHTNSYCLQGIQSNQRTGNDADANEMRVEELPGLESVVGVL EELVMWPSRY  
 PTIFNASPLRNQAGVLLYGPPGTGKTYLVSQLATSWNLRIISVKGPELLAKYIGQSE  
 ENVRNLFNRARSARPCVLFFDEFDSLAPKRGHDSGTGVTDRV

15 >15:26:30|GENSCAN\_predicted\_CDS\_1|5457\_bp|  
 gaaatggtgcaggcaaaaggatccgccctcacattacttgagtaaaactgcgcacatatctggacccaaaggcatcaaggagtcate  
 ggctttatctcttactttctgtcagaaacggaaaatggcggcgagtcacgtccacccaggtgctccgcgatctggagatctc  
 gctgcgcacgaaccacatcgagtgggtgaaggagttcctggatgacacgaaccagggctggacgccctggcgcactatctcag  
 ctccgactgcagatgatgcgacacgagcagcgccctcaggggtgtctgtgtgcctcggaggagcgtctgaatctcacaacggc  
 20 ggcgatggcggtgagatagtgatgggaaacagtagttctgttagtcctgggtggaggtgggtgttactatcacatgaaacagtac  
 gggacatggctggccaatggcacacttgactcgaggcagcagcacacaatgtcctatggattcctacgacctaccattgccgat  
 gctctggatagtcctagtgtgaagcgaagggtcacgacatatggccaaattaacatgggtgccgccacggacgacatccatgtgtc  
 cattatgtgcctgcgagctatcatgaacaataagtatgggttcaacatggttatccagcatcgcgaggccatcaactgcattgccttg  
 agtcttatccacaatcgctgaggacgaaagccctggctcggagctgctggcagccatctgtctggtaaagggaggacacgaa  
 25 atcattttgggttcgttcgataatttaaggatgtgtgccaggagaagcgacgcttccaaacgctcatggagtactttatgaacttga  
 ggcccttaacatagattttatgggtgcctgcagtcagttcatgaacatcgttgcactcgggtggaggacatgaactacaggggtgcac  
 ttacagtacgagtttacgccctgggcttgataagtatctggagcgaattcgattgacagaatcgagggaactgaaggtgcagat  
 atcagcctatttgacaacgtctttgatgttgctgccttgatggaggattccgagacaaaaacttcagccctggaacgagtcgaaga  
 gcttgaggatcaacttgagcgagaaatagatcgtaactcagagttcctctataagtatgcggaattagagtcgagagcttaacgct  
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 35 atgctaagctccttcaaccgccaccgcctccagtggcggctttatgccgctcccgatggcgccatgacctcaaacgcaagg  
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 gttagaacacattgcaatctcccgtcgcaagctgggtatgcccattgatgatgtcatcgccgccattcatagcttgacctgaagaa  
 40 actttccctggagaacgtcgagctgctgcaaaaaatgggtgccacggatgccgagggtcaaatcctacaaggaatatatcatcgag  
 cgcaaggaccaacagctactcaccgaagaagacaagttatgctgcagttgtcgcgtgtggagcgtatctcgtccaagtagcca  
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ttaagcaacacgatcaggagaacgagcagcgtcttcgcctggaaaaggccgctgcgctggccgctccaagaaagagaacga  
 tcaggtgcttatgcgcaacaaggtaaccagaagaagcaacaggaagctgtcataaacgagctgaagagcaaggcgactcgg  
 tgcgcgagaaaaagctgctgcagcaggacgaggtgtacaacggagccctggaggacatcctgctcggcctgaagagcgagcc  
 gtacaggcggcgatgctgtgcggcggtgcagcgcgggaggtatcacaataatcgttatcgcgcaccctggaggaaatgg  
 5 attgctgcacgagaatgatctggtaagtgtgcgctcatcgtgacgttctcaacctgcgcagcgtccacgttaccctcgtcgt  
 ccaaggactgggagatcatagaacttagcactgaaaagatatcgggcagtgtgctggaacaaactgcatagtgaattcaacgca  
 gatecttattgttggattaataagtcgatgcaagttgcgctgacagtggatcgtctgaagccgcacatgaactacgggagaataga  
 tcacaatacggaaactcgtggtggcgcccaatctgtacaagggtctgaccaatggaactcaaatggtgttatagggaaaacacaa  
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 10 aatgtgaaaaatactattcagcgtacaagcgtcaggatcacatggagcgtcttaaaaaggacttgcgccggaagctcgcgta  
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 gaacgcatttaagcgaattgtgatagagagaactcagcacaaagccgatgctcttcaaccaggaggaggtggtacggctggagga  
 cgatttactggttactgttgaattttaccagaacactttcgttattgcgtggtggacgcgcagtttctgaaggagtcgaagatctacg  
 cagcagatcgtgtgcgtccggttggcgagattattaaggaggagacgctccgacatcgcactaaagtgttcaggatctcatcca  
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 20 cagtgcattgtctactcgtcgtggtgcctcgggaacgggtaaaacagttcttgtggagcgcattttggaccagctgtcacgcaagcc  
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 aggtatggagagtactacaatcgcgtgactgtgtatcagttgattgttcagtataccaccaacaacgctattgcagtaatcg  
 ccaccgtcaacgagttgcagaccctcaataagcgattgagctcaccaaggggaagacatgtcttcagactgttgctcgtctgcc  
 25 aatttgaacgagcagatcgagagataattcttcgagagctgtgcagccatatcaatgtggccaaggacctggatcttgaagtct  
 ccaacctcacggagggtaccggaatgtgatctgttcagttcgtggagcgtgcaatattttatgcttatcgcataagcaagacc  
 agcctcttctgaccaatgatcagcttattgagtcctggagcacacaaactgtactgcctgcagggcattcagagcaatcaaga  
 actggcaatgatccgatgccaatgaaatgcgcgtcaggaggtgctggcctggagtcagttgtgggagttctggaggaggtcc  
 ttatgtggccatcaaggtatccaaccattttaacgcctctccactgcgcaaccaggccggagtactctatatgggccaccaggaa  
 30 caggtaaaacctatctggtctctcagttggccacatcgtggaacctgcgcacattccgtcaagggtcctgagttgctcgccaaata  
 tattggtcaaacgcgagggaaaatgttcgaaacctgtcaatcagctcgcagtgcccgaccatgtgtgctttcttcgacgagttgac  
 agcttggcgccgaaacgtggtcacgattccacgggggtcaccgatcgagtg

**Drosophila Gene Hit** recue sequence and TBLastn with ORF1: mRNA for l(3)70Da (AJ243811)

35 **Human Homologue** BLASTX with l(3)70Da: peroxisome biogenesis factor 1 (AF026086)

**Drosophila EST** LD43687 ( AI512050)

40 **Annotated Drosophila genome genomic segment** AE003536

**Annotated Drosophila genome Complete gene candidate** CG6760 mRNA for l(3)70Da  
 - novel protein with  
 homology to endoplasmic  
 45 reticulum ATPases

**Human homologue of Complete gene candidate** 4505725

ref[NP\_000457.1|pPEX1|  
peroxisome biogenesis factor  
1 >gi|2655141 (AF026086)  
(8e-80)

5

**Putative function** Putative member of the AAA protein family (ATPases associated  
with diverse cellular activities) including homologies to  
transitional endoplasmic reticulum atpases, and an E.coli  
membrane-bound AAA-type metalloprotease which degrades  
degrades sigma32, an alternative sigma factor for heat shock  
promoters

10

**Confirmation by RNAi** Slight loss of G1, increase in G2/M indicating arrest in  
G2/M

15

**Line ID** 238/44  
**Category** Meiotic defects in testis: segregation defects, multi-stage defects (PI-02/18)

**Reversion** R  
**Map Position** 70D

**Rescue ID** F8E

**Rescue Sequence**

10 GTTCAAACGCACCTTTTAAGGTGGCCTATCGGCCCATCAGGAGCAACTTTGTTC  
 TGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGG  
 TCTTCGCTCCATTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTCT  
 GATTAGGACACGGGCTGCCTGAGCTTGCAGTACAATGGTCGGACGCACTACG  
 CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG  
 15 GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCGG  
 ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATTTGCCCCG  
 TACCTCGTACGCTAGCAGCACCCACTTACCCTTTCTTGCCGTATGTCTGCACGA  
 GAATGATCTGGTCAAAGTGTGCGCT

20 Other results same as for line 238/37

**Line ID** 428/5  
**Category** Meiotic defects in testis: cytokinesis defects, segregation defects (seg-01/01)

25 **Reversion** ?  
**Map Position** 70A

**Rescue ID** G4E

**Rescue Sequence**

30 GTTCAAACGCACCTTTTAAGGTGGCCTATCGGCCCATCAGGGAGCAACTTTGTT  
 CTGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAG  
 GTCTTCGCTCCATTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTCT  
 TGATTAGGACACGGGCTGCCTGAGCTTGCAGTACAATGGTCGGACGCACTACG  
 CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG  
 35 GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCGG  
 ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATCTGCCCCG  
 TACCTCGTACCTAGCAGCACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGAA  
 AATGATCTGGTCAAAGTGTGCGCTCATCGCTGACATTCTCAACCTGCGCA

40 Other results same as for line 238/37

**Line ID** 848/7  
**Category** Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defect. Multi-stage defects  
 Polyploidy, no overcondensation  
 5 **Reversion** PI-01/10  
**Map Position** R  
 70D1-2

**Rescue ID** G1E

10 **Rescue Sequence 1**

GGCCACCTTAAAAGTGC GTTTGAACATTCTCGTCGTGGGCGTGTGCGAATTTA  
 GTACGCTCCTTCCTGGTTTAAATCATTTTCGCACTAAACTTCTGCTCTCAGCGG  
 AATTTACTTTTGCTTTATTAGAGATGGGAGCTCGCGCATCAGCTGAGCCGATA  
 CTTGCGCAACAGGTGATACAGCTGATTAGAGATGGCCCTTTTCAACTGTTCCC  
 15 AGCAGTGACCGCTGCCATAACCGTTTTTCAAATTTACGTGAGAACAGACATAA  
 AATAAATATTACAGCTCGTAGTAAATGTTATTCTATATTTAAAAGGAAATTGT  
 AATAGTTAAAACTTGCAATGAATCAGTTACGTTCAAAAAGGAAACACACTTT  
 AGTTTTTGGCTAGTTTATTGGGTAAATAATTTTTATTTAAAATAGTTTCGAGTG  
 TTCAATATAGTCATGTAAATGTGTACAGAAAGATCCGGCATTGATATTTAAT  
 20 ATATCGATTTCCCTTCACCTTCGCTCCTCGTATACCATGCTGGGGTCTTATCAA  
 ATTTATT

**Rescue ID** G1P

**Rescue Sequence 2**

25 AAGGTGGCCTATCGGCCCATCAGGAAGCAACTTTGTTCTGCTGCCGGATCAGT  
 ACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGGTCTTCGCTCCATTCAA  
 ATTAGATACGCCAAAGATTAATCCGGTCAACCATTCTGATTAGGACACGGGCT  
 GCCTGAGCTTGCAGTACAATGGTCGGACGCACTACGCCTCCTGGGCGCCACAA  
 AAGGGCGGCGGCGGCATTAAAGACACCGAGATTGGGATCAATGCCACAGCGG  
 30 CCAAGGAGATCGGTAAGCCATTACTTAACGGCCGGATGTGCATCGGTTGCCAA  
 TGTGCCGTAATATTGGACTCCGGCCATCTGCCCCGTACCTCGTACGCTAGCAG  
 CACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGAAAAATGATCTGGTCAAG  
 TGTGCGCCTCATCGCTGACGTTCTCAACCTGCACAGCGTCCACGTTACCCCCGT  
 CTCGTCCAA

35

Other results same as for line 238/37

**Example 37 (Category 4)**

**Line ID** 252/40  
**Category** Meiotic defects in testis: segregation defects, abnormal spindles.  
 5 (Ab-03/30)  
**Reversion** R  
**Map Position** 84E

**Rescue ID** A4B

10 **Rescue Sequence 1**

TACATGACTCTGCGATTTGACAAAAACAAAATTGAGTTTTGTCAAGAAAATCA  
 ACTATTTTTCTGTGTTAAAAAACCGAAGCCAACAAATCCGACCAAAATGCCT  
 GCCGAAAACCTGGAGGAGCAGGGTCTGGAGAAGAACCCGAACCTGGAGCTGG  
 CCCAGACGAAGTTCCTGCTTACCCTGGCGGAATACAAGCAGGATGCGGCATTG  
 15 AAGGCGAAGCTTCTGGAGGCGATTGCGACGGAGAATATGGCCCCGTGGGTAC  
 GAGCACATCCTGCTCCGGAACCTCGGCTTGGACCCGTTAGACAAGGATCTTGCC  
 TGGCGCCGAATTGAAGGAAAAACAATCGCGTTTAAGTTGGGAGCCA

**Rescue ID** A4E

20 **Rescue Sequence 2**

GTCATGTACTACCAGTGTGACCCCAAAGTTATCGATAAATTATACCGCATATT  
 TTAACATTGCCAAAAATACCAGAGCGATGTCCATCAAGATAGCGACGAAATT  
 AGAACAGTGCAATTGCCAATTGGGAATTTGTATTTTAATTTATTTTTAAATTCT  
 GAAAGTAATTTTAATTTAAAAAAAACCTTGAGAGCTGTCTAGAAAAGAACTTAT  
 25 GTTTCATGATAACTTTGTGCGAAGAATTAAGAAATATTTAGTTGTAAAATAATT  
 GTNTGAATCTATTTTTTTTCCAATAACACGACTTATATTTTTTTTTTAAATATTC  
 CGAGCTAAATCCCAAGAAAGTTAACTCCAATCTTGGGATTTTGAAGTGCCCC  
 AGAACTCCAAATTAAACACTTCCTTTTTTAAATAATTGTTAAGACCCGTATCA  
 CTTATGGTTATATACTGACCTCGAAAGGGCCACACTAAGGGGGGAGTTTGAAA  
 30 ATTGATTTTCCTGATAAAAATTTTCGCTTGGAAAGCTACAGCATCGTCCACTGTC  
 CATGTTTATATATCCTTATATTTGCCTATAAATATAT

**Genomic hit, Accession No.** AC006494

35 **Associated ORF**

Genscan: ORF1 predicted sequences >23:00:28|GENSCAN\_predicted\_peptide\_2|389\_aa  
 MPAENLEEQGLEKNPNLELAQTKFLLTLAEYKQDAALKAKLLEAIRTENMAPWY  
 EHICSELGWTVDKDLLARMKENNRVEVEQLDAAIEDAEKNLGEMEVREANLKKs  
 EYLCRIGDKAAAETAFRKTYEKTVSLGHRDLIVFHLIRLGLFYLDHDLITRNIDKA  
 40 KYLIEEGGDWDRRNRLKVYQGVYSVAVRDFKAAATFFLDTVSTFTSYELMDYPT  
 FVRYTVYVAMIALPRNELRDKVIKGEIQEVLHGLPDVKQFLFSLYNCQYENFYV  
 HLAGVEKQLRLDYLIHPHYRYVREMRLGYTQLLESYRSLTLQYMAESFGVTVE  
 YIDQELARFIAAGRLHAKVDRVGGIVETNRPDNKNWQYQATIKQGDLLLNRIQKL  
 SRVINI

45 >23:00:28|GENSCAN\_predicted\_CDS\_2|1170\_bp

atgcctgccgaaaacttgaggagcagggcttgagaagaacccgaacctggagctggcccagacgaagttcctgcttaccct  
ggcgggaatacaagcaggatgcggcattgaaggcgaagcttctggaggcgattcgacggagaatatggccccgtgttacgag  
cacatctgctcggaaactcggctggaccgtagacaaggatctgctggcgcgaatgaaggagaacaaccgcgtagaggtggagc  
5 agctagatgcggcaatcaggatgcgggagaagaatctgggcgagatggaagtgcgcgaggcgaatcttaagaagtcagagta  
ctgtgccgcatcggcgacaaggctgccgcagagactgccttccgcaagacctacgagaagaccgtttccctgggtcaccgcct  
ggacatcgtgttccatctgatccgcttgggactgtttaccttgaccacgatctcatcactcgcaacatcgacaaggccaagtatctg  
atcgaggaaggcggcgattgggaccgacgcaaccggtgaaggctaccagggtgtttactcgggtggcggtgcgtgacttcaag  
gcggcggccacgttcttctggacaccgtaagcaccttcacatcacgaactgatggactacccaccttcgtgcgttacaccgtt  
10 tacgtggccatgattgccctgccgcgaatgagctgcgcgacaagtgatcaagggtccgaaatccaggaggtgctccatggc  
ctgcccgacgtgaaacagttcctgtttcctgtacaactgccaatatgagaacttctacgtacacctggccggcgtagagaagcaa  
ttgcgcttgactacctcattcatccccactaccgctactacgtgcgcgagatgcgcattctgggctacaccagttgctggagtcg  
tatcgtccctcaccctgcagtatatggccgagtcgttcggcgtaacagtgaatacattgaccaggagctggcacgcttcatcgc  
cgccggacggctgcatgccaaggtggatcgcgttggcggcattgtggagaccaatcggcctgacaacaagaactggcagttacc  
15 aggcgaccatcaagcagggcgatctgctgctcaaccgcatccagaagttgagccgcgtgataaacatctaa

**Drosophila Gene Hit** BLASTN with rescue sequence 1 and TBLASTN with ORF1: 26S  
proteasome regulatory complex subunit p42A (AF145308).

**Human Homologue** BLASTX with EST and TBLASTN with ORF1: Hypothetical  
protein KIAA0107 (D14663).

**Drosophila EST** several including GH17651 (AI387197)

**Annotated Drosophila genome genomic segment** AE003739

**Annotated Drosophila genome Complete gene candidate** CG5378 - Rpn7 19S  
25 proteasome regulatory  
particle, non-ATPase protein,  
subunit S10aHuman  
Homologue

**Human homologue of Complete gene candidate** gi7661914  
8843E6684AE91ACD  
30 [ref]NP\_055629.1| KIAA0107  
gene product [Homo sapiens]  
(3.40E-149)

**Putative function** component of the 19S proteasome regulatory particle

**Confirmation by RNAi** Marked decrease in G1 and G2/M indicating fewer cycling  
40 cells

**Example 38 (Category 4)****Line ID** 277/7**Category** Mitotic defects in brain: anaphase defects  
(weak, higher condensation, some polyploidy, fewer anaphases,  
polyploids with monopolar spindles)**Reversion** ?**Map Position** 71B**Rescue ID** B8E**Rescue Sequence**

AGTCGGCGCATGCGGAGAGAGAATCGAAAAGAGAAAGAGAAGCAAAGAGAGC  
 GACATACAGCAAAAACAATTCAAAAAGAACTGGTGAAGAATACGAAAATAAG  
 ATAATTTTTTAAGGAAGTCGCGCTTTGATCCGTATCCGTTTTAGCGTCCAAGAT  
 TTATATCTTAAATCGGACCTATATTTTGAGGTACAGTGAAGCTTTGATGCGCCA  
 GTCTTATATGAGTTAAAGTTTTAACGATTGAAAGACACCCCTGAGCTGCTCAT  
 TATATTTCAATATTTATAAACAATCTTATATCAGAGCTTGAGAGACTTGCGATGC  
 GCCACAAAATTCCAATTCCAATTCCAATCCGGAATAATTTACAATAATCTC  
 AATTAACATACGTATTTTATGTTTCGTAATTTTTTAAAATTCCCAGATTCCCCAC  
 AATTGCCATAATAATCTCGATTATGTTATTATACTCTGAGAAGTAGGAGTGTG  
 TGCAAAGACCACAAACAAATCATTAGGGGCGT

**Annotated *Drosophila* genome genomic segment** AE003584**Annotated *Drosophila* genome Complete gene candidate** CG15383 – novel**Human homologue of Complete gene candidate** none**Putative function** No homologies to indicate function**Confirmation by RNAi** Slightly increased G1 decreased G2/M indicating arrst in G1

**Example 39 (Category 4)**

5	<b>Line ID</b> <b>Category</b>	284/4 Mitotic defects in brain: anaphase defects (overcondensation, polyploidy (with overcondensation), few anaphases, metaphase with bipolar spindle)
10	<b>Meiotic Reversion</b> <b>Map Position</b>	NR 89B
10	<b>Rescue ID</b> <b>Rescue Sequence</b>	2C6E GTCTACCACTAGCTCTTTGTCTTCGCCTTCTAGTCTCTCTCATCTTGGCAGCCC GTTCTAGTGCGCGTATTTTTAGTCGCAACACATTGCCCAATTGCCCAGCCGCTA 15 TTTGTGTCGTCCATTTGTTTCATTCATCGGGCTCTTTTCCGATTTTCAGTGGGTGG CATTTAACAATAATCCCTGCGTTCGCTGTCCACGTCCACATTACGATACGTTTA GTGCACGGAAAGAAATAAGCGTGTGGTTTCATAATATTAGCTATTGAAAAAA GTTCTTAAATTTAAGCCTCACTCGATTCTGATGCATGAAATATTATTGGATTGT AAATGAGCGTCATGTTTTGGTATACAAATCTCAAAGTAATTTAAAAAATTCTCA 20 TCTTACCGTACCTTGAACCACTACCAATCATCTCAGTACAGCATTTCAGCGAA TTTCTCACTGTGCACTACAATGCCAGGCGGTACAAGCACCTGTATTTATTTATG GTCCGCTGCCGTAATCGACTGCAGTCGCCGCTTCCCTCTCTCTTTTGCTACCAA CAACTTGGGGTAGGGCACCTGAACTAGTTTCAAACGGCGGCGGTTCGGCCTTTT CAGCTTTTTTCGCATTTGCCATTTTCCCGCGG
25	<b>Annotated <i>Drosophila</i> genome genomic segment</b> <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	AE003711 CG4275 - mor transcription factor involved in chromatin remodelling
30	<b>Human homologue of Complete gene candidate</b>	CG4275- 4507081 [ref]NP_003066.1 pSMARCC 2  SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2(aa)
35	<b>Putative function</b>	Transcription factor, regulator of chromatin
40	<b>Confirmation by RNAi</b>	Decrease in G1 and G2/M and increase in polyploidy

**Example 40 (Category 4)**

**Line ID** 407/8  
**Category** Meiotic defects in testis: cytokinesis defects  
**Reversion** ?  
**Map Position** 64B1-2

**Rescue ID** A9E

**Rescue Sequence**

10 GACTCACCCTTTTCACGCATTTTCATTGGAACGTTTGTTCGTTTATGCACACGC  
 GTGTTGACACTTTTCATGAAACGCAGTGCCTGAAAAGTGCATCGCATAAACGC  
 AATAAATGTTTGATGGATGCGTTCTGATGGCTTGAAGTCGCCTATTTGGCCGA  
 TTTTCGCACGTCCACTCCCGACGGCAACAGAGTCCTGACTGAATCCCGGAGCG  
 GAAGGAGTGTGGATAGCCAGGACTGCCAAAGGACACTGCGCACTTTTACTTTT  
 15 TCGAAAGCGAAAGCGAAAGTGGTGGGGCCCAGGCCAAAACAANCCCTTGAGT  
 TGAAATTGGAAAAAAACCGGGACAGGGATGGGAGCCCAGCTCCAACAAACG  
 GTTCCGGATTTCCTTGGGAAAGCCACGCCCTGCGCCTGGAAAAGGAATGCCCTC  
 CACCTCATTTGTCTCCGTTTTGCGCTATCTCTCCCCCAAATTTCCGTTAAATG  
 AAAACAACCTTTGGGTTTTTGGTTTTTAACAATTTCTCCCCATTTGGTTTTNNGG  
 20 TTCCCTTTCCATTTTGGGAATTGGTTTTAATTAAAT

**Genomic hit, Accession No.** AC005814 64A6-64B6

**Associated ORF**

25 Genscan ORF1 predicted sequences >22:57:22|GENSCAN\_predicted\_peptide\_2|524\_aa  
 MGRRKDKPRVIPEQDARICRAICLCQLTMVLSCVSIVYLSVAIYSPSLKAFKSGFEL  
 DPVMCQTVDRQMPNCPWASCGEWCLTKTSGFCPQIHSIVRRNGTDIQLNNCTR  
 VTNTSCAMIDLSRLNKFNCNNGTACNNIRGVFNCSNGHCKNMSEFFLCHHKADG  
 LTVNSQKDNTKLNFFFECHGVHCTKIKKPFSCDRYCSKITTTNVNTLIMHEDNLIA  
 30 ADCENAVAFNQARGSEHGVRIEPFEFWKEDDGNLLTNCATVTRESNRRITATDCI  
 NGTLLEHDTLPAPFMNFTQFWAIYENSTRSVDPEQRYLPNQANLTIYSWKKLFINL  
 EGCVNTRLRGECKDFVARYGNDGDNNTAQSRVQCYYNKDSNVEFVVARYDLDK  
 VYRELLVSLIVPIVLFISSISLCIITKSVKVGDDAKMRCVCAGDDSDNDGPFPGPL  
 ANKQQDQMYDTHDDVVDLEHQAVDGGQELSDHGLPLDNQELIGSTKSLIPSPVGE  
 35 SGTSDQIFDQDQEKATTCDVPEKPLVIL

>22:57:22|GENSCAN\_predicted\_CDS\_2|1575\_bp

atggggcgccgcaaggacaaaccgcggtgattcccgaacaggatgcgcgcacatctgtcgcgccatctgcctgtgccagctgac  
 catggtgtctgtctgtgtccatgtctacctaagcgtggccatctactgcctccctaaaggccttcaagtcgggtctgagct  
 40 ggatcccgtcatgtgccagacggtggtatcgccagatgcccaacaactgccctgggcatcctgcggcgagtggtgctgacca  
 agaccagtggcttttccccagatccactcaatagtcgctgcgaacggcaccgatccagctgaacaactgcaccagagtcac  
 caacacatctgcgcctatgattgacctgagtcggctgaacaagtcaattgcaacaacggcaccgcctgcaacaatatcagaggc  
 gtcttcaactgctcaatggacactgcaagaatatgtcggagtcttctgtgtcaccacaaagccgatggacttacggtcaattcgc  
 agaaggataacaccaagctgaatggattcttcagtggtcacgggggtgactgcaccaagatcaagaagcccttcagctgcgatcg  
 45 ctactgttccaagataacaactaccaatgtgaacacccttattatgcacgaggataatcttattgccgccgattgtgagaacgcagtg  
 gcttcaaccaagcccaggatccgagcacgggtgtcgtatcgaaccctttgagtttggaaaggatgatggcaacctgctga

ccaactgcgccacagtcacaagagagtcggacaatgcacactgccacggactgcataaatggaaccctcctggaacatgaca  
 ccttgcccgcctcccttcacgaacttcacccagttttggggccatctatgagaacagcaccaggctcggtggatcccagcagaggtag  
 ctgcccaccaggccaacctgaccatctacagctggaagaaactgttcacacacctggagggtgcgtgaacacactgcgtggg  
 5 gagtgcaaggactttgtggctcgcctatggcaacgatggcgataacaacacccagtcacgctaccagtgctactataacaagg  
 actcgaatgtggagtttgggttgacgctacgatttggacaagggttacaggaggcttctagtctcgtgattgtgccattgtgctc  
 tttgtgatctcatctatatcggtatgtatcatcaccaatccgtcaagggtgggtgacgatgccaagatgcgctgtgtttgtgccggcga  
 tgattcagataatgatggccccttggcccaggactagcaacaagcagcaggatcagatgtacgatacagacgacgatgtagtt  
 gacctggagcaccaagcgggtggatgggtcaagaactatcgaccacggacttcgctggacaaccaagagctaatacggtagcac  
 caagtcgttgataccaatcagtcgccgtcggaagaatcggaactagtgtatcaaatcttgaccaggatcaggagaaagcaactacgt  
 10 gcgatgttcccagaaaaccactagtcatactataa

(corresponds to CG15003)

15 **Annotated *Drosophila* genome genomic segment** AE003480  
**Annotated *Drosophila* genome Complete gene candidate** CG15003- novel unknown

**Human homologue of Complete gene candidate** none

20 **Putative function** No homologies to suggest function

**Confirmation by RNAi** Only wild type profiles observed

**Example 41 (Category 4)**

**Line ID** 422/28  
**Category** Meiotic defects in testis: segregation defects, multipolar spindles  
 5 (Mul-02/22)  
**Reversion** NR  
**Map Position** 68E  
  
**Rescue ID** 2I4E  
 10 **Rescue Sequence**  
 TCGTGGACCCTCAAAGNAACGGATTTCTCCAGTTTCTTCAAAGGGTTAATAAAA  
 CTTTTCGCACGTTTCGCATTTTTATGCTCAATCCGGTTACAAAATGCTGATAAA  
 ACCACTTGAACACACGTTTCCGTACTGATAAGGGCTTTTCTTCTTATCTGACC  
 TCTGGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCGTGATACGCC  
 15 TATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCA  
 CTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATT  
 CAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT  
 TGA AAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATCCCTTT  
 TTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTA  
 20 AAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCT  
 CAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAA

**Genomic hit, Accession No.** CSC:AC014962

25 **Annotated *Drosophila* genome genomic segment** AE003543  
**Annotated *Drosophila* genome Complete gene candidate** CG5684 (putative  
 transcription factor, human  
 homolog  
 30 **Human homologue of Complete gene candidate** 1e-100 4758946  
 ref|NP\_004770.1|pPOP2|  
 POP2 (yeast homolog)  
 >gi|4106061|gb|AAD02685|  
 35 (AF053318) CCR4-associated  
 regulator of polymerase II  
 transcription

40

**Putative function** Transcription factor

**Example 42 (Category 4)**

**Line ID** 422/5  
**Category** Meiotic defects in testis: segregation defects, abnormal spindles  
5 **Reversion** ?  
**Map Position** 82D

**Rescue ID** B9E

10 **Rescue Sequence 1**

ATTGGCTCTTGATGGACTACAACGCTACCAAAATGGGGCTTGAGTTGAATTAC  
CTGTTGGAAGACACAATGCCACCCACGATCAACAATTCGGCGGTAAACAGTG  
CCGCCGAAAAGCGACCCAGCGGCAAACGGGAGCGCAAGTAAGTGAACAGAT  
CCCTAAACAGACCCAGATACTCAGACTGATGTGTACCTTGCAGATCCGAGATC  
15 ATTTGCCGCGTGAAGTATGGAAACAACCTGCCGGATATACCATTGATCTGAA  
GTTTCTGCAGTACCCCTTCGACAGCCACCGCTTCGTGCAGTACAACCCAACGT  
CGCTAGAGCGTAACTTCAAGTATGACGTGCTGACGGAACACGATTTGGGTGTC  
ACGGTGGGACCTGATTAACCGGGAGCTCTATCAGGCCGACTCCATGACGCTGC  
TGGACCCGCCGATGAAAAACTGCTGGAGGAGGAGACTCTGACGCCACAGAC  
20 TCTGTGCGTTCGCGCCAGCATTCGAGGACGGTGTCATGGTTGCGCAAATCCGA  
GT

**Rescue ID** B9B

**Rescue Sequence 2**

25 GGCCAAATCTAGAAATCCTCAAATCTGCGCTTGGCAGTGTGACCGTACTTGAC  
CGGTACGATAATACCTCCGGTAAAAAAAATACTATATTTCCGGGGGACTCAAA  
TGCAACATCCTCATCGTATATAACACAACATCTATTTGAATTTTCATTTCCACAA  
CTAATATTATGGATAATGCTTTATTATCATTTTCCAAGTTAGCGATAAATCACC  
CCACAAGCTGAAAAATCAACGTTTAAAAACGATTGATATTTTTTTTAATACTTT  
30 TTGGTTTTACTATTTGAATTTTTGTATACTTTTAGATTTTACTATTTTAATTTTC  
GTTTCTTCTAGCTGACTAACGGGTAAAAAAGGATCCGTGACCTGCAGATCT  
CTAGAAGCTTGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGC  
ATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA  
AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCCGTGCGCTCTCCTGTTCCG  
35 ACCTGCCGCTTACCGGATACCTGTCCGCCTTCT

**Genomic hit, Accession No.** AC008189

**Associated ORF**

40 Genscan ORF1 predicted sequences >15:53:24|GENSCAN\_predicted\_peptide\_3|211\_aa  
MRNANESSGKPKSKFVSNEFHAFSTICSIA DSPAVSREKLKIDLAARKIPSASAPK  
GDSPLERFSRDLFTYLRVCRWGRFSAALFTAELLIVGGIVSSNRTSESSETGNPLA  
NEPDPLYMKLVDP MVAGESPKRM IKDQKDVGLKSTSSSEELRKLPKTRGRQKRFI  
RNP NYVKANEFYDKMLSSEYVSKRYKDLPPHPGFGADQPPA

45 >15:53:24|GENSCAN\_predicted\_CDS\_3|636\_bp  
atgcgcacgcacaaatgaatcgagcggttaaccaaatacgaattgtaagcaacgaattccacgcattgtttcaacaattgttcaa

ttgccgattccccggctgtctctcgagaaaaattgaaaatcgatttagctgctcggaataaccttcggcatcagccccaaaggg  
gatttccactcgagcgcttttcgcgggatctgttcaacttacttgcgtccgtttgcccgtggggtcgcttttcggcggcactgtttacc  
gccgaattgttgatcgtgggtggcattgtgtcttccaacagaaacgtcagagtccttctgaaactggaaacccacttgcaaacgagccc  
gatccattatatatgaaactgggtgatcccatggtagcaggagaaatcacctaaaaggatgattaaggatcagaaagatgtaggcctt  
5 aaatcaactagcagtagcgaagagctccgaaaattgccaaaaacgcgaggtcgacagaagagattcattcggaatccaaactat  
gtgaaagctaacgaattctatgataagatgttaagcagtgaatacgttaagtaagcgggtataaggatctccgccgcctcatccggga  
tttgagcggatcaaccgccagcatga

Corresponds to CG2503

- 10 **Annotated *Drosophila* genome genomic segment** AE003605  
**Annotated *Drosophila* genome Complete gene candidate** CG2503 - novel possibly  
RNA binding
- 15 **Human homologue of Complete gene candidate** 3287674 AC005239  
(AC005239)  
F23149\_1(aa)

**Putative function** Possible RNA binding protein

20 **Confirmation by RNAi** Almost no G1 and broadened G2/M indicating arrest in  
G2/M

**Example 43 (Category 4)**

**Line ID** 423/14  
**Category** Meiotic defects in testis: cytokinesis defects, abnormal spindles  
 5 (Ab-16/13)  
**Reversion** R  
**Map Position** 67B1-10  
  
**Rescue ID** E9E  
 10 **Rescue Sequence**  
 GTTTGGCGTAAAAGCTTCGGCTGTGTTTGGTGCCCAAATTTTCCACTGCTTCT  
 CTTTTTGTGTATCTCTTATATCTTGTGCTTTTTTGTGTGTATGTTTTCTCGTTTC  
 TTTTGCACACGCGCTTCGCGTTGCGGGCCAGCTGTTTTTGTGATAAGTGGT  
 TACGGTTTGTGTGTGCCAGCGGGTTTTCCTTAGTCGAACTGCTCGCGATGACTG  
 15 ATTTTTCACAAGTGACTCAAAAACAGTCGATCGCCCTTTTAAGAAAACCCGCT  
 CAACGCACACAAAAGCGGTTTCTCTCTTTTGTGCTTCTCTCTTTTCACACTGA  
 CCACACGGAACGAAAAAATGATTACCGACCACACGGAAGAAAAATTTATGT  
 CCAGACGAAACTATTTTGTCCAAGCTGATTTGCATAACAATTTAAGCCA  
 CAAGAACTAGATTAAAATTTTACATTAAATACATTATCAAATCCGAAATAT  
 20 CAATAATTGTAATTTATCCTTACAAAATGTTA

**Genomic hit, Accession No.** CSC:AC020214

***Drosophila* EST** several including LP12306 (AI297868)

25 **Annotated *Drosophila* genome genomic segment** AE003552  
**Annotated *Drosophila* genome Complete gene candidate** CG3967 - novel

**Human homologue of Complete gene candidate** none

30 **Putative function** No homologies to indicate function

**Confirmation by RNAi** Only wild type profiles observed

**Example 44 (Category 4)**

**Line ID** 427/5  
**Category** Mitotic defects in brain: anaphase defects. Meiotic defects in testis: segregation defects, abnormal spindles  
 5 (mitotic : Overcondensation, lagging chromosomes/less aligned metaphase with bipolar spindles, Meiotic: Ab-06/20 )  
**Reversion** ?  
**Map Position** 67B1-5

10 **Rescue ID** H4E  
**Rescue Sequence**  
 GTACAGCCTGAAGTGATCGTTGTTGTTTGAATCGGTGCTATCGGCGGTTGCGC  
 TTTGTGGGCATCTTTATCCAATTTGCTATGCGCGCTTGTCCTTAAATTTTGAAC  
 TGTATTCCAAGGGTTGCTTTGGCGGCTATCGATAGTATCGGCATGGTTACATTT  
 15 TAGTTTTATAACAAGAATTTTACAGGTATTTTGATTATCTGAGCTTAGTTTTAA  
 GCAANAATATTATTGTTAAAAATTTAAAAAGTAAACAAGCTATTTTAAACAAGC  
 ATTTAAACAAATAGTATTAATAATATAAAAAATATATCGATATGTGTTGCAAAT  
 GTTCGTTCCCTTAGTATTCTCTCATATTTATTTCAAATAAACTGTATAAAATAT  
 CTGAAAAAGCGAACATATTTATTTAATTTTCATCGCAGATATCGATATCACAGC  
 20 GCTGCTATCGATGGTGTGTCTGTCGCAGTGCCTATCGCTTACCCTGCCATCGCT  
 AACAAAAA

**Genomic hit, Accession No.** CSC:AC020120

25 **Associated ORF**  
 Genscan: ORF2 predicted sequences >22:06:07|GENSCAN\_predicted\_peptide\_7|464\_aa  
 MPSEQHTNIKVAVRVRPYNVRELEQKQRSIIKVMDRSALLFDPDEEDDEFFQGA  
 KQPYRDITKRMNKKLTMEFDRVFDIDNSNQDLFEECTAPLVDAVLNGYNCSVFV  
 YGATGAGKTFTMLGSEAHPLTYLTMQDLFDKIQAQSDVRKFDVGVSYLEVYNE  
 30 HVMNLLTKSGPLKLREDNNGVVVSGLCCLTPIYSAEELLRMLMLGNSHRTQHPTD  
 ANAESSRSHAFQVHIRITERKTDTKRTVKLSMIDLAGSERAASTKGIGVRFKEGAS  
 INKSLLALGNCINKLADGLKHIPYRDSNLTRILKDSLGNCRITLMVANVSMSSLT  
 EDTYNTLKYASRAKKIRTTLLKQNVLKSKMPTEFYVKKIDEVVAENERLKERNKA  
 LEAKATQLERAGNSGFDPLELKTWYSKIDAVYAAARQLQEHVLGMRSKIKNINY  
 35 RQTLKKELEEFRLKLMCVDQRCQESF

>22:06:07|GENSCAN\_predicted\_CDS\_7|1395\_bp

atgccttcggaacagcatcacgaatataaaagtggcggttcgcgtacggccgtataatgtccgtgaattggagcaaaaacagcgga  
 gtattatcaaggatcatggtcgttcggcactgctgttcgatcccgacgaggaggacgatgagttcttcttcagggcgccaagcaac  
 40 cgtaccgcgacatcaccaagcggtgaacaaaaagtgaccatggaattcgacagggtattcgatagacaattccaaccagga  
 tctgttcgaggagtgcacggcgccgctggcgcacgggtgtaaatggatacaactgctcggtattgtatatggagccactggcg  
 ccggaaaaacattcacaatgctgggcagcgaggctcatccgggtctgacctattaccatgcaagatctcttgataagatcaa  
 gcgcagagcgacgtgcgcaagtcgatgtgggggtatcctatagaggtgtacaacgaacatgtgatgaatctgctaactaatc  
 gggccctttaaacttcgcgaggacaacaatggcggtgggtcagtggtcttctcacgccatctacagtgcgaggagctgc  
 45 taagaatgctgatgctgggcaactctcatcgactcagcaccacacagatgccaatgcagagagttccaggtcacatgcatcttc  
 caggtgcacattaggatcacggagcgcaagaccgacacaaaagaacgggtcaactatccatgatcgtctggcgggcagtgga  
 gggggcgccagtagcgaaggcattggagtgcgattcaaggaaggcgccagcatcaacaaaagtcttagcttgggaattg

cataaacaagctagccgacggcttaaagcacatcccgtaccgcgactcgaacctgacacgcacccctgaaggactcgttgggcgg  
 aaattgtcgacattgatgggtggccaatgtctcgtatgagctcactgacctatgaagatacctacaacacccttaagtacgctagccg  
 agctaagaagatacgcacgactctgaaacagaatgtcctcaagtccaagatgccaaaccgagttctatgtgaagaagatcgacgag  
 gtggtagccgagaacgagcgactcaaagagcgcaacaaggcgctggaggccaaggccactcagttggagcgcgccggcaat  
 5 agtggattcgatccgctggagcttaagacgtggtacagcaagatagacgctgtatatgcggccgccggcagcttcaggagcac  
 gtccttggtatgcgtagcaagatcaagaacatcaactaccggcagacactgaaaaaagaactggaggagttcaggaagctgatgt  
 gtgtcgaccagcgagtggtgccaggagagtttttaa

***Drosophila* Gene Hit** TBLASTN with ORF2: kinesin like protein 67a (U89264)

10 **Human Homologue** TBLASTN with ORF2: kinesin family member protein KIF3A  
 (AF041853)

***Drosophila* EST** GH22018 (AI402731)

**Annotated *Drosophila* genome genomic segment** AE003552

15 **Annotated *Drosophila* genome Complete gene candidate** CG10923 Klp67a -  
 motor protein

**Human homologue of Complete gene candidate**

2e-58 4758646 kinesin family  
 protein 3B

20 >gi|3913958|sp|O15066|KF3B  
 \_HUMAN KINESIN-LIKE

PROTEIN KIF3B and also  
 predicted peptide  
 ENSP00000166696

25 Gene:ENSG00000073652  
 Clone:AC015936

Contig:AC015936.00023  
 6.70E-91 (predicted kinesin?:  
 ENST00000166696)

30

**Putative function** motor protein involved in cytoskeleton organization and  
 biogenesis

35

**Confirmation by RNAi** Almost no G1 and broadened G2/M indicating arrest in  
 G2/M

**Example 45 (Category 4)**

	<b>Line ID</b>	442/3
	<b>Category</b>	Meiotic defects in testis: segregation defects.
5	<b>Reversion</b>	?
	<b>Map Position</b>	70D4-7
	<b>Rescue ID</b>	H7E
	<b>Rescue Sequence</b>	
10	CGCAAGACTGTCTTCGATAGCAGAAGCGTTATTTTCGGAACATATCGTTTATCG	
	AAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTCAA	
	ACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAATT	
	AAAATATAAACTACGAGGATCAAATATACATACATATTCCCAATATGTTAGCG	
	AAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTCTA	
15	TGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTTCA	
	ATTTAAATATATTTTAATATATTCAAATATAGTATAGCAGTATAGCATTCAAAT	
	GTAAGTGTGGTTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTCATC	
	GCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATTA	
20	<b>Genomic hit, Accession No.</b>	CSC:AC017664
	<b><i>Drosophila</i> EST</b>	CK02287 (AA141680)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003536
25	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG6650 - novel transacylase like
	<b>Human homologue of Complete gene candidate</b>	none
30	<b>Putative function</b>	Transacylase
	<b>Confirmation by RNAi</b>	Marked increase in G1 indicating arrest in G1
35		

**Line ID** 473/22  
**Category** Meiotic defects in testis: no division  
 (no meiosis)  
**Reversion** R  
**Map Position** 70A1-5

**Rescue ID** 2B7E

**Rescue Sequence 1**

CGCAAGACTGTCTTCGATAGCAGAAGGCGTTATTTTCGGAACATATCGTTTTAT  
 CGAAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTC  
 AAACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAA  
 TTAATAATAAACTACGAGGATCAAATATACATACATATTCCCAATATGTTAG  
 CGAAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTT  
 TATGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTT  
 CAATTTAAATATATTTTAATATATTCAAATATAGTATAGCAGTATAGCATTCAA  
 ATGTAAGTGTGTTGGTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTCA  
 TCGCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATAAGAA  
 AGTTGGCGTAGCCGGAAGGCGGATTGTCACATACAAAATAGTTTGGAAAGCC  
 CAAACTGAG

**Genomic hit, Accession No.** CSC:AC017664  
**Drosophila EST** LD47104 (AI515336), SD03663 (AI532240)

For other results see line 442/3

**Line ID** 670/6  
**Category** Meiotic defects in testis: segregation defects, abnormal spindles  
 (Ab-12/48)  
**Reversion** ?  
**Map Position** 70C

**Rescue ID** H7E

**Rescue Sequence**

CGCAAGACTGTCTTCGATAGCAGAAGCGTTATTTTCGGAACATATCGTTTATCG  
 AAACACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTCAA  
 ACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAATT  
 AAAATATAAACTACGAGGATCAAATATACATACATATTCCCAATATGTTAGCG  
 AAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTCTA  
 TGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTTCA  
 ATTTAAATATATTTTAATATATTCAAATATAGTATAGCAGTATAGCATTCAAAT  
 GTAAGTGTGGTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTGTCATC  
 GCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATTA

**Genomic hit, Accession No.** CSC:AC017664  
**Drosophila EST** CK02287 (AA141680)

For other results see line 442/3

**Example 46 (Category 4)**

5	<b>Line ID</b> <b>Category</b>	460/20 Meiotic defects in testis: segregation defects, multipolar spindles (mitotic: High polyploids, no diploids, higher mitotic index Meiotic: Mul-02/59)
	<b>Reversion</b> <b>Map Position</b>	NR 78A1-4
10	<b>Rescue ID</b>	2B8E
15	<b>Rescue Sequence</b>	AGCTGGTCCAATTGGAAACGTTAGCTGCTCCAATGGGAGCAGCTGGCGCTCTC TCTTCGATCGCGCTCGCTCTCATCCTCTCTCTTTAGCTTGTGCCACAGTAGCTG CCGAAGGCAATTTTCATGTGCTCGTGTGTCGACCCCCACTCAGCCCCACTTCTG ATCGGAATCGGGGATTTCGGAATCGTGTAAGGCAGCCTTTGAAGGTCCCTTTTC CAGGTGGCGGCCGTATCCTTAAAGTAAACATAGTTCAACTGACTTGGCAGCGC TCCAAATGCGGTGACTTCTTGGCTATGTCATATATACCCCCACTCCCCTCCTGA CTACCCTGCCACGCCCCACCGCCACCGTCGGCGACGACAATTCCATTAAAAG TTGTACGTTGTCACTTTGCGTTAACTTATCTGTGGAGCATGTTGTGCGATCGCA TTTTTATTGTCGCCATTGTCTCTCGCTCTCTCCATCGCTCTTTCGCCTGGCTTCC CTACCCTGCCCACACAGGGAAGCCTACACACTCTTAAATCATGCACTTGGAAAC AAAAAGTGCAAGCATTAACCTTTATTTAAACATTCAAGAGCCGCTTCTCTATT TACCATTGAAAATTTAATTTAAAATAGAAGAGGCCTTTTCAGAATAATATAAT ACCTTTAAG
25	<b>Genomic hit, Accession No.</b>	CSC:AC020460
30	<b>Annotated <i>Drosophila</i> genome genomic segment</b> <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	AE003592 CG10588 - novel gene with homology to proteases
35	<b>Human homologue of Complete gene candidate</b>	2e-74 4505453 ref[NP_002516.1 pNRD1  nardilysin (N-arginine dibasic convertase) >gi 2462488 emb CAA6369
40	<b>Putative function</b>	Novel protease
	<b>Confirmation by RNAi</b>	Marked increase in G1 indicating arrest in G1

**Example 47 (Category 4)**

**Line ID** 477/16  
**Category** Meiotic defects in testis: segregation defect.  
**Reversion** NR?  
**Map Position** 90C5-10

**Rescue ID** C3E

**Rescue Sequence 1**

10 CTGTGGACGGTCGTCAATGCGTGAATATTCTTCTATGTGTAAGTGGTGTGCGT  
GTATGTAGATTTCTGGTTAAGAAAAGCCCCAAAAACCAAAGCGCCCCGAAA  
ATATATATTGAGTCTTCTTGGCCCAACAACAAATCTGCCGCCGGACTTTCGCC  
GGAGGGCGAGTGAAAAATTCAGTTTCTCTCCTCTCGACGATGCACTTTGGAGG  
CTGTGTGAGTGTGTGTGCGAGTGAGTGCGTGTGTGTATACATATGCAAATGAT  
15 TGGATGTGCAATCCTTGCATCATCATCTTCATAAACACTTGGCGAAAAAC  
CGCAGGAAAACGCAAGCAGCCGAACAAAAAAGAGAGCCTCTCAAGACAAC  
GGCAGCGGCCAAAAGTGAACGCGCAACAAACGCGGCCAAGCAGGCGCGGCA  
ATTATTTATAAATCTTAAGCCGTTAGCCCCCTCTCTCTCCCACTCACGAAAAG  
AAAATAAGTTAAACCAATTGGTGAAGATGATGCCCC

**Rescue ID** C3P

**Rescue Sequence 2**

25 GTCCACAGACTGGCTATATATACTAAAAACGAACTCGCGTGAGAAGACAGGG  
ACAGGGCAGCAAACCTCGGTATACGAACGGAACGAAATGAAACGATTCAAGTA  
GTAGTGTATGCAAGTCTTGTCTGTCTGCGCCTGGCGTTCTTTTCTCTCTTTTT  
TCGATGGTTTTTCGCCAGGCTGGGCGCTGCCAAAACGCTGATACGGCGGCCAC  
AATCACACGCGGCTAATCGCCAGTTGGGCCCTGCACAGGCTGCACATACTTTT  
CACTATTAATGCGCTGTATTTCACTTATTTTTTCGAACAAATTCGCAGCATGACG  
AAGAAGCGAGCCTGTACAAGATTAGAGCGGGTAGCACGCACGATAGTATCGA  
30 TACGTACGAGTATTTGGCACTGCGATACATTATCGGTGCTCGTTTCGATAGCCC  
CCGATAGCTCTAGCACGAAATTTTATCGCTTTATCCATATTTTATACTATTTTT  
ATTTATTGGACTTCAATGAATATTTAATTTACGTCTGGGTCGCTTTTAAATAT  
ATATGGTAATCAATAGCTGGCGAATTAGCGATATTTGAGTGTGACGCAAAAAT  
GAGTTGCATCGATATCGATTTCTCGCTACTCTGGGACGCCATCTTTATTGCGG

**Genomic hit, Accession No.** AC007810

**Associated ORF**

40 Genscan ORF1 predicted sequences >17:48:58|GENSCAN\_predicted\_peptide\_2|349\_aa  
MSRILFILLLLIVTQLSELQAAAFSVRQNRFDVPLQTPAPLATSTESSKKPEKAT  
SGLLKKCLPCSDGIRCVPIQCPAHVRMESHEKPQICDLPAGKFGYCCETGQNHT  
APKPETSPKERRSGFPTILSPA VLDEARRNFEHLMHGVAQIPVRRGFDPFAHGLVF  
HSTAKDDLHNFAISNSAJEQVMTTQLFGKKEQVPVEDFITNNVPIKFTETPLAHHC  
QPPPVCGNIRSVYRSMGTCNNPEPQRS LWGAAGQPMERMLPPAYEDVPSASPA  
45 AICSYIYGIASRLAPVSVVNCCTFAWQLDWTGTMASGECVCVECMPEAWRLGQC  
PLLHEASSEMSRLLAKS

>17:48:58|GENSCAN\_predicted\_CDS\_2|1050\_bp

atgagtcgcaattttattttgttgcacttattgtgacgcaactgagcaggttcagggcgagcattttctgtgcgcaaaatcggt  
 ttgatgaagttcctgatttgcagactcctgcacctctggccactccactgaattcttaagaaacccgaaaaagctaccagtgggt  
 5 gctgaaaaaatgccttcctgcagcgcgtgataagatgcgtgccccaaatccagtgtcccgccacgttcgcatggaaagccat  
 gaaaagcccaaatgtcgatctcccggtggaaaattcggctactgctgcgagactggacagaatcacactgctcccaagccg  
 gagacctctcccaaggagcgcgcgatccggattcccaccattctgtcaccgcagtttggatgaggcgcgctcgcaatttcgagca  
 ctgatgcagtgagttgcgcagattccgggtgcgcgtggcttccagatttggccatggcctggtttccactcgacggccaaggat  
 gaccttcacaacttcgccatcgaacagtgcattgaacaagtgtgaccaccagttgttgggaagaaggagcaggtgcccg  
 10 tagaagatttcacccaacaatgtgccatcaagttcactgagactccgctggcacaccattgccaaccgccccagtttgcggc  
 aatattcggtctgtttatcgagcatggacggcacttgcaataatccagaaccacagagatctctgtgggtgctgctggtaaccg  
 atggagcgcagctgccccccgctatgaagatgttcgcgcagcttctcctgctgctatatgtagtatatctatggcatcgcatctg  
 tctggcgctgtttctgttgaattgttgacattgcatggcaattggattggaccactggaatggcgagcggggagtggtgtgt  
 gtggaatgtatccggcgagtggtggttggccaatgccgttgcctcatgaggcgtcgagtgaatgagccgcctcttgcta  
 15 aaagctag

**Drosophila Gene Hit** rescue sequence: eyelid/osa (AF053091)

**Human Homologue** BLASTX with eyelid: KIAA1235 protein (AB033061) Brain  
 protein 120 (AB001895)

**Drosophila EST** several including LD04852 (AA201670), LD24466

**Annotated Drosophila genome genomic segment** AE003718

**Annotated Drosophila genome Complete gene candidate** CG7467 - osa DNA binding  
 putatively involved in DNA  
 packaging

**Human homologue of Complete gene candidate**

CG7467 - 7e-25 2588991  
 dbj|BAA23269| (AB001895)  
 B120 [Homo sapiens] and  
 O14497 SWI/SNF-  
 RELATED, MATRIX-  
 ASSOCIATED, ACTIN-  
 DEPENDENT REGULATOR  
 OF  
 CHROMATIN SUBFAMILY  
 F MEMBER 1 3e-67

**Putative function** transcriptional regulator

**Confirmation by RNAi** Only wild type profiles observed

**Example 48 (Category 4)**

<b>Line ID</b>	496/4
<b>Category</b>	Meiotic defects in testis: segregation defects, abnormal spindles (meiotic: Ab-08/42)
<b>Reversion</b>	NR
<b>Map Position</b>	65E4-7
<b>Rescue ID</b>	2C1E
<b>Rescue Sequence</b>	<p>GCACGATCGCTCTCTCTTGGCTCTCTCTATCACTCTCTGGACTCTCTCTCAGCA  CCTTTGCTACCGTTTCGCAGAACAGGTGTATCGGTTTTCAAGGCAACTGTGATT  TTTTAACTCAACATTCTATATCGAAAACCTTGTAGAGGTCGGAATTTTTCTTGAG  CGCCTAAAAGTGTGCAGTGAAATCATTTAATCCACTTCCGGTTGCAAAACAGG  AATCACACATATGAAGTGATTAAAAATCATAGAAGGTTTGACACCTTCAAATA  ATAAGAAAACAAAAATTTGTAACTGTGATAATTTATTTAATTGAAATCTTAA  TTTAATGGCCTACAAATCTGTTGAATATCCGTTGAATACACTTTTCCAGGGTGT  GTCCTAGTCGGCTCCTCTTTGTTACCCAGTTTGCTGGTCTTCTTAGCCGCACA  CCAGTTTATCGCTGTTTGCCTTTGCGCTTTTCATTTCATAAACAAAAACAATG  TTATTGTTATTGCGGTGGCTGTAGATGTAAATGTAAATGTAGATGTAGAGGCT  GCTTCTTGGG</p>
<b>Genomic hit, Accession No.</b> CSC:AC018039	
<b>Associated ORF</b>	<p>Genscan ORF1 predicted sequences &gt;19:35:36 GENSCAN_predicted_peptide_6 190_aa  MVSEQFNAAEKVKSLTKRPSDDEFLQLYALFKQASVGDNDTAKPGLLDLKGKA  KWEAWNKKQKGSSEAAQQEYITFVEGLVAKYDNGMHKQEPNTCQARNATFR  KSSECSLDQNTYTSSVTVIPAFHEGPKNSTASWPRIYRCYQRNQQAAANCKWANTN  SVCCKPHGKQSRRIFAEFLAGHTVQILG</p>
<p>&gt;19:35:36 GENSCAN_predicted_CDS_6 573_bp  atggttccgagcaattcaacgccgccgagaagggtgaagagcctgaccaagcgtcccagtgatgacgagttcctgcagctg  tacgccctgttcaagcaggccagcgttggtgacaacgacaccgccaagccgggtctcctggacctgaagggaaggccaagtg  ggaggcctggaacaagcagaagggaagagcagcggagccgccagcaggagtacatcaccttggaggggcctgggtggc  caagtatgacaatggaatgcacaaacaagaacaaacacttgccaagcagcaatgcgactcggttcgaaaagctcgaatg  ctcgctggatcagaatacgtatacgtccagtgtagcgttatacctgcattccacgaaggtccaaagaactcgacggcaagtggc  caagaatttacgggtgctatcagcgggaaccaacaagcgccaactgcaagtgggcaaacacaaatagcgttgcgggaaaccc  cacggaaaacagagccgccgaatcatttcgcagaatttctggccggccatacgggtgcagattcttggttaa</p>	<p><b>Drosophila Gene Hit</b> rescue sequence: melt (S144114) P element insertion site  (AF174669), TBLASTN with ORF1: diazepam binding inhibitor  (DBI) (U04823 ) and melted (AF205831)</p>
<b>Annotated Drosophila genome genomic segment</b>	AE003560
<b>Annotated Drosophila genome Complete gene candidate</b> CG8624 melt - putative signal	

		transduction protein
		CG8631 msl-3 - acyl-CoA-
		binding
		protein/diazepam binding
5	<b>Human homologue of Complete gene candidate</b>	inhibitor
		CG8624- predicted gene
		ENSP00000065899
		Gene:ENSG00000055889
		Clone:AC015904
10		Contig:AC015904.00014
		1.70E-15 (unknown predicted
		gene 1: ENST00000065899
		and AK022666 Homo sapiens
		cDNA FLJ12604 fis 2e-29
15		
		CG8631- gi5803104
		0C85AE40FDF874CD
		[ref]NP_006791.1  male-
20		specific lethal-3 (Drosophila)-
		like 1 [Homo sapiens] (1.70E-
		36) and Ensembl predicted
		peptide ENSP0000006617
		Gene:ENSG0000005302
		Clone:AC004554
25		Contig:AC004554.00001
		8.70E-19 (unknown predicted
		gene 1: ENST0000006617
30		
	<b>Putative function</b>	CG8624: putative signal transduction protein
		CG8631:acyl-CoA-binding protein/diazepam binding
		inhibitor
35		
	<b>Confirmation by RNAi</b>	CG8624: reduced G1 and G2/M Indicating fewer cycling
		cells, CG8631: Increased G1 to G2/M ratio indicating arrest
		in G1

**Example 49 (Category 4)**

5	<b>Line ID</b> <b>Category</b>	523/19 Female sterile. Meiotic defects in testis: cytokinesis defects, segregation defects (Mitotic: Less condensed chromosomes, nuclear bridges, Meiotic: Seg-01/02)
	<b>Reversion</b> <b>Map Position</b>	R 75C1-4
10	<b>Rescue ID</b>	2B4E
15	<b>Rescue Sequence</b>	ACTGAGAGCATATTTGTGCACCAGAGGGCTGCATAACAACATTCTCTTTGTCC ATTCGTTATACTTCGTATTCAGAATACATGTCATTTCAGTTGGTCCCGTTCTTTT GCGTTCACCTTCGTATATATTCGGCGATCGAAATGAACTAACTGAATGTGTTCA AAGAATGAATGAAGCCAATGAATTTTCAATAGTAATTCAGAGTGCTTAAAATT CTTCATGTTGTCATTGAGTAAAATGAGTTCGGACAGCGCGAAGGTAAGTCGAA GTTTGTGTTTTATTATGTTTATTTGTATTATTATGTACACTAGTCGGCATACTTT TGCGTGCGTCTTATACGTGTGCGTCTTATTTAACAATATTGTAAAATAAAATAT ATAAATTATTTGTTATATGCGTAGGGGCCTTTATTTTGTGTATTGATAGTCTTTT GTCATAGATATCATTATTCTGACAAGATTTGAACTTTTCAAGTTATTGCCTCTC GTTATTCAATTCCTAGCTGGTCTTACGTTACGCGATATTTCTTAAAATATCCTA AAATCGCACAAAACAGTCACGCCACACTTTTGAAAAACGTGGTAATATTTT CATACTTGCAATTAAGTCTGG
25	<b>Genomic hit, Accession No.</b>	AC007691
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003520
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG4306 – novel
30	<b>Human homologue of Complete gene candidate</b>	4e-25 3242764 (AC005154) similar to protein U28928 (PID:g861306) [Homo sapiens]
35	<b>Putative function</b>	No homologies to indicate function
	<b>Confirmation by RNAi</b>	Only wild type profile observed

**Example 50 (Category 4)**

**Line ID** 666/19  
**Category** Mitotic defects in brain: anaphase defects  
 5 (weak, overcondensation, aneuploidy, lagging chromosomes, metaphase with bipolar spindle)  
**Reversion** NR  
**Map Position** 64E1-5  
 10 **Rescue ID** I9E  
**Rescue Sequence**  
 CCCTCGTCTACGTCGAAATTCTGGATGCTTCTCGGATTTAGGGTTGTATCTCGA  
 AAACGTTTGACTGCGAATGTCAATATCGATATGCTAACCGATAGCTGTTCGATG  
 TTTTAAACACAGTGCACTGTTTTTAAATCGCTCCCCATTTATATATATTTGTGC  
 15 NTGCTTTTGGCGGTNNTTTTCTTTATATGCTTCTTATGCTTTTACGATTATTATT  
 AGCGCTTATTTGATTGCAAATGCCAAGGAAAGCGTGACTGTGATGGCGAAATG  
 CGGAAAGTACTCCTTAAATCTCATATATCGCATAAAACTATCGGTTCTGGAAT  
 GTTTCGTGTAAGTCTGCGAAGATAGAGATCGATCTATTTTGAGGATACATTTG  
 TTAATATTATAAGGGATTCTTCTACAGGGGTCAGATTGCTTAAAAACACACAG  
 20 AANAATAAACAAAATATTTCTTTGAAATATTGAAATATTTGAAATANAAAAAA  
 CGTATTGACGAGGTAAGCATATTGAAAAAGATAGGAAGGTGATGGAGAAAGT  
 GCACTTATATTGGTCACCAAAGAGCTTATAATCAAAAGATCAATAGATATAAA  
 TATCTTTATATGATATAAAATATAATACATATAATATAATATCATATACAATG  
 GATAAATTGCAAGTGGCAAAATGAATTCGCGGAATTAATTCTGAANCGAAA  
 25 GGGCCT

**Genomic hit, Accession No.** CSC:AC014815

**Associated ORF**

30 Genscan ORF1 predicted sequences >17:46:43|GENSCAN\_predicted\_peptide\_1|334\_aa  
 MGKDFYKILGLERKASDDEIKKAYRKLALKYHPDKNKSPQAEERFKEIAEAYEVL  
 SDKKKRDIFDNYGEDGLKGGQPGPDGGGQPGA YTYQFHGDPRATFAQFFGSSDP  
 FGAFFTGGDNMFSGGQGGNTNEIFWNIGGDDMFAFNAQAPSRKRQQDPPIEHDLF  
 VSLEEVDKGCIKKMKISRMATGSNGPYKEEKVLRITVKPGWKAGTKITFPQEGDS  
 35 APNKTPADIVFIIRDKPHSLFKREGIDLKYTAQISLKQALCGALVSVPTLQGSRIQV  
 NPNHEIHKPTTTRRINGLGLPVPKEPSRRGDLIVSFDIKFPDTLAPSLQNQLSELLPN

>17:46:43|GENSCAN\_predicted\_CDS\_1|1005\_bp

atgggcaaagacttctacaagattctgggcctcgagcgcaaggccagcgacgatgagatcaagaaggcctaccgcaaactggc  
 40 actcaaataccatcccgacaagaacaagagcccacagcgaggagcgcttcaaggagatcgccgaggcggtacgaggtgctg  
 tcggacaaaaagaagcgcgacatcttcgacaattacggtaggagtgattgaaggcgcgacagccgggaccagatggcggcg  
 gtcagccgggagcggtacacttaccagttccacggcgatccgagggccacattgccagttcttggatgctcgatccgttggc  
 gcgttctttaccggcgggcgaatacatgttagtggcggtcaggcgggcaataccaacgagatcttctggaacattggcggcgacg  
 atatgtttgccttaatgccaggcaccagtcgcaagcgccagcaggatccgccatcgagcatgatctgttcgtgctgctggag  
 45 gaagtggacaagggatgcatcaagaagatgaaatctcacgcatggccaccggaagcaatgggcccgtacaaggaggagaag  
 gtgctgaggatcacagtgaagccgggctggaaggccggtaccaagattaccttcccccaaggagggtgattcggcgccaaaca

gacgccagctgacatcgtcttcattcgcgacaaaccgattcgtgttcaaacgcgaggggaatcgatctaaagtatacagccc  
agatcagctctgaagcaggccttgtgctggagcactggtagtggtgccacgtgcagggcagcaggatacaggtgaatccgaacc  
acgagatcatcaagcccaccacaacgcgcccggatcaacggactgggtctgccggtgcccaggagccatcgaggcgcggcg  
atctgatcgtctccttcgacattaagtgtcccgacacactggcaccagctctgcagaatcagctgtccgagctgtgcccactag

**Drosophila Gene Hit** rescue sequence: fasciclin I (FasI) ( M32311) TBLASTN with  
ORF1: DnaJ homolog (DROJ1) (U34904)  
**Human Homologue** TBLASTN with ORF1: DnaJ-like heat shock protein 40 (HLJ1)  
(U40992.2)

**Annotated Drosophila genome genomic segment** AE003565  
**Annotated Drosophila genome Complete gene candidate** CG10578 - DnaJ-1 a  
chaperone putatively involved  
in protein folding. Stimulates  
activity of HSP70

**Human homologue of Complete gene candidate** 8e-94 1706473 P25685  
DNJ1\_HUMAN DNAJ  
PROTEIN HOMOLOG 1  
(HDJ-1) (HEAT SHOCK  
PROTEIN 40) (HSP40)

**Putative function** Chaperone involved in protein folding

**Confirmation by RNAi** Almost no G1 peak, increased G2/M indicating G2/M arrest

**Example 51 (Category 4)**

**Line ID** 714/11  
**Category** Meiotic defects in testis: cytokinesis defects, abnormal spindles  
 5 (Ab-01/04)  
**Reversion** ?  
**Map Position** 66A10-15

**Rescue ID** 2A4E

10 **Rescue Sequence**  
 AACCAGAACGAACTCCAATGCAGTTTCATTTTGTCTAGTTTAATCATTAAACA  
 AAGAACTGCGCAACCGATCGCAACTAGCTCGTGGACTCTTGTTCTCCCAATAA  
 TTGGTATGTTTTCCATTTTGCCTTAACATGGAAAATGTGTGAAAAGCTTTTTCC  
 CCCTCCAAAAGAAGCGTACTGAACTAAGCTTTCGGTGGTTAGTAATAGTAGTC  
 15 GTTATATCTTATTTTCTTATTTACGTGCAGCTGCAATCATTGGCTGCGTCACTT  
 TGGCGTCAGCTATAAACTGGTGGATCAACTCGGCGGCCTCCAAAAGCTGCGCA  
 TCTGCTCCAGACACTTTAGCCAACGCCAGGAGATGGCCAAAACCCGCATCAA  
 GATGACGCCGCTGCGCAAGTCCTCGTCTCCAAGGGCATTGTGCTACCCATTA  
 ATGCCGCTGGAGGGTCGGTTCATTGCAGGCGCCTTAGCACGAGGAGGAGGTGC  
 20 A

**Genomic hit, Accession No.** AC012390

**Associated ORF**

25 Genscan ORF1 predicted sequences >19:47:45|GENSCAN\_predicted\_peptide\_2|711\_aa  
 MRSHQAVGNLLLADEALPAVQSASVYVWMAEQPLSPGQSYDIKIADSPSVSS  
 KSITDNGADVQWFAFEHSQYYQGVQQMFLSALERIDSEFLITLIKRCPHYVDSLVSQ  
 LSEVCKMTEDFSLASELLERALLLLESSLHINFSLTSGNCRLDYRRQENRSFYIVLF  
 KHAQYLEERACSRTAFEISKLLLSLQPDTPDLAMILPNQPDQCTGNMTQLQQAGK  
 30 IRKRSEKQFPITGTEPRGTDALRFTLQTLASAGRDITWNIKRLQGSRTVGAQAQGYLI  
 DKKTAVQYKITIIAHLKDPNIDQLFDSSGDGKADLHGSTPDWGCQAMMADAISR  
 YKEGNPVFYITWTPYWVSNELKPGKDVVWLQVPFSALPGDKNADTKLPNAGGI  
 EGLIADDEEVQVLDALCDAPCVGVSHSCRLLDGNRRGNNELRLFIPGKSQFGVADG  
 CADKQSVMEYHAAKTGHTKFSESEEEKKALTEEEKKAQLALIEEKLKQKRIEREE  
 35 REKIEALQREKNRIKSGKDMTEAKRRMEEMKKIVEQRKREKDEEKAARDRVK  
 AQIEADKAARKAREQKELGNAEPAPSVSSTTVSSPPAGVKSPPRDYTETRIQGASA  
 ILAAAAPYYQPPAVPQDVQPDPIGYGAFGVVCGSHISGWHCSAGHYEDGNENFE  
 CLKTFSTSDRIGCEWRWAAATVLAATCISPNGRCGHYKRVRRRIKTNITTT

40 >19:47:45|GENSCAN\_predicted\_CDS\_2|2136\_bp  
 atgagatgcacatcaagccgttgcaatctgctgctggcggcagacgaagcgttacggcggtgcagagcgcgctcggtgtatgtg  
 gtatggatggcgggaacagccgctttctccagggcagagttacgacatcaaaattgccgactctccatcggtgtctccaagtctatc  
 acagataatggagcggacgttcaatggttgctttgagcatagccaatactaccaggagtgacgcaaatgttcctttctgctctcg  
 agcgcattgactcgggaatttctgacacacttatcaaacgctgcccctatcatgctgactccttggttcaactcagcgaagtatgcaa  
 45 gatgaccgaagacttttcttgccctccgaactgcttgagcgcgcccttctccttctggaatcgtcgtgcacatcaacttcagtttga  
 cgtcgggcaactgccgactggactaccggagacaggaaaaccgatccttctacatcgtgctgttcaagcacgcgcagttacctgg

aggaacgagcttgcagccgaccgccttcgagatctccaaactgctcctgagttcagccagacacagatcctcttgcattgatt  
 ctaccaaatacagccggatcaatgtaccggcaatatgacgcagctgcagcaggggcaaaatccgtaagcgtcagaaaagca  
 gtttccgatcggactgaaccgcgcgggtactgacgcgttgcgcttcacacctgcagacactggcgctctgccggtcgcgacatcacct  
 5 ggaatataaagcgtctgcaagggtcccggtgtaccggcgccgcccagggttacctcatcgataagaaaaccgccgtccagtacaa  
 aatcaccatcatcgctcatctgaaagatccgaatatcgaccaactgttcgattcaagcggcgacggaaaagcggatttacacggta  
 gtaccccagactggggctgccaagctatgatggccgacgccatcagtcgctacaaagagggaacccgggttttattacacctg  
 gacggcgtactgggtgagtaacgaactgaagccgggcaagatgtcgtctggttgaggtgccgttctccgactgccggggcga  
 taaaaacgccgataccaaactgccgaatgccggtggcatcgaaggcctcatcgccgatgaagaagtccaggtcctcgatgcct  
 ttgtgatgcgcgtgtgttggtgtctccactcgtgcccactccttgatggcaatgccgaggggaataatgaactgcggctctttatt  
 10 cccggcaaatccagtttgagtagctgatggatgtgcagacaagcagagtgttatggagtaccatgccgcaaaaccggtcac  
 accaaattctccgaatcgaggaggaaaagaaggcgctcaccgaggaggagaagaaggcccagctggccctcatcgaggag  
 aagctcaagcagaaacgcacgaacgcgaggagcgcgagaaaatcgaagccctgcagcgggaaaagaatcgcatcaagtcc  
 ggcaaggacatgaccgaggccaagcggcgcatggaggagttggagatgaagaagatcgttgagcagcgcaagcgcgaaaa  
 ggacgaggagaaggcggcccgcatcggttaaaggctcaaatgaggcggacaaggcagcacgcaaggctagagaacaaa  
 15 aggaattgggcaacgcagagccagctccatccgtgagctccaccacagtttcgtcaccaccggccggtgtgaaatctccgccgc  
 gagactacaccgaaaccgcacccagggcgccagcgcaatcttgccgcagcggctccctactatcaaccgcccgtgttccc  
 caggatgttcagccggatcgtcctatcggtatggagcattcgagttgtctgcggttcccatcagcggctggcattgttctgcg  
 gggcattatgaagatggtaatgaaaatttcagtgcccaagacatttcgacttctgaccgcattggctgcgaatggagatgggcg  
 gcagcaactgttcttcgccgaacctgcattagcccgaacggccgttgccggcattataaacgcgtacgtcgtcgattaaaaacaaa  
 20 cataacaactacgtga

**Drosophila Gene Hit** rescue sequence and BLASTX with EST: BIP1 (Y14998),  
BLASTX with genomic sequence matches BIP.

**Human Homologue** BLASTX with BIP1: alanine:glyoxylate aminotransferase  
(X53414) ?

**Drosophila EST** GM04749 (AA695904), GM13608 (AA803601)

30 **Annotated Drosophila genome genomic segment** AE003556  
**Annotated Drosophila genome Complete gene candidate** CG7574 - bip1 unknown  
 function

CG13681 – unknown

35 **Human homologue of Complete gene candidate** none

**Putative function** no homologies to indicate functions, Drosophila Bip1 interacts with  
transcriptional activator Bric-a-brac which is required for ovariole  
formation

40 **Confirmation by RNAi** Both show reduction in G1 and G2/M indicating fewer  
cycling cells

**Example 52 (Category 4)**

<b>Line ID</b>	763/4
<b>Category</b>	Meiotic defects in testis: segregation defects (overcondensation, fewer anaphases)
<b>Reversion</b>	R
<b>Map Position</b>	90F
<b>Rescue ID</b>	2F5E-1
<b>Rescue Sequence</b>	<p>CGGCAATGTCTGCGCCCCCAATCTGAACTTGCCTCGCCCTCTCCGCCCCCTGATC  TCATCTCCTCTTCAAACCCCTGCTCCCCCTTTTCTGCACACATTAACGTCAGCCT  TTAAGTGTGCTTTCTCAGGTGCTGCCCCCTGCGCCCACCATCCCCCGCTCCATG  CTCTTTCCATCTTTCGCTCTCTGCGTTCTATCTACATTTTTTTCGAGGTCGCGCG  CTGCTTTTTCCGTTGATGTTTCGTTCTCGTCAATGTCGCAATATGCGCAAAAGGC  AGACAAAAAAAAAATGAGTGGAAAAAGTACATACATACCGGTGATTGATGGG  CGGTGGGTGGCGGTGGTGTAGGNGTGGTTTG</p>
<b>Genomic hit, Accession No.</b>	AC006495
<b>Associated ORF</b>	<p>Genscan ORF1 predicted sequences &gt;22:47:02 GENSCAN_predicted_peptide_3 283_aa  MTERENNVYKAKLAEQAERYDEMVEAMKKVASMDVELTVEERNLLSVAYKNVI  GARRASWRIITSIEQKEENKGAEKLEMIKTYRGQVEKELRDICSDILNVLEKHLIP  CATSGESKVFYYKMKGDYHRYLAEFATGSDRKDAEENSLIAYKAASDIAMNDLP  PTHPIRLGLALNFSVFYYEILNSPDRACRLAKAAFDDAIAELDTLSEESYKDSTLIM  QLLRDNLTLWTSDMQAEEIPIPKLPDRQSKTTLIFSPRSQVNPILHKNNTIIGRVIC  SVFA</p>
<b>&gt;22:47:02 GENSCAN_predicted_CDS_3 852_bp</b>	<p>atgactgagcgcgagaacaatgtgtacaaggcaagctggccgaacaggccgagcgctacgacgaaatggaggagccatga  agaaggtcgctccatggacgttagagctgaccgtcgaggagcgaatctgctgtcgggtggcgtacaagaatgtgattggagcac  gccgtgctcgtggcgcatcatcacctgatcgaacagaaggaggagaacaaggggggcgaggagaaattggagatgatcaa  aacctaccgcggacaggtggagaaggagctgcgcgacatctgctcgatatactgaacgtgctcgagaagcatctcattccatg  cgccacatccggcgaaagcaagtaattctactataagatgaaggggcgactaccatcgctacctggccgaattgccaccggctcc  gaccgcaaggatgcggcagagaactcgtgattgcctacaaggcgccagcgatattgccatgaacgatctgccaccaacaca  ccccatccgtttgggcttgccattgaactctcgggtgttctactatgagattctcaactcgccggaccgcgcttgccgcttgccgaaa  gccgctttcgatgatgccattgccgagttggatacactgagcgaagagagctacaaagactcgacactcatcatgcagctgctgc  gcgacaacctcacattatggacgtcgatagcaggcagaagagattccgattccaaaactccccgacagacagtcacaaaacca  cattgatttttagccccgaagtcaagtaaacccaaagattctccacaagaacaacaccatcatcggcagagttatctgtagcgtgtt  tgcgtga</p>
<b>Drosophila Gene Hit</b>	rescue sequence: 14-3-3 epsilon isoform gene (U84898) TBLASTN with ORF1: 14-3-3 .
<b>Human Homologue</b>	TBLASTN with ORF1 and BLASTX with 14-3-3: epsilon isoform 14-3-3 protein (U43430.1)

	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003721
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG8045 complex gene
5		appears to encode 3 things : Transcript: CT24102 unknown Transcript CT24072: transcription factor RNA polymerase II transcription factor ,
10		Transcript: CT24092: diacylglycerol- activated/phospholipid dependent protein kinase C inhibitor /14-3-3 protein
15		epsilon (suppressor of ras)
	<b>Human homologue of Complete gene candidate</b>	CT24092: e-119 NP_006752.1  tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, epsilon polypeptide; 14-3-3 epsilon [Homo sapiens
25	<b>Putative function</b>	transcription factor, or 14-3-3 proteins which associate with cdc25 phosphatases
	<b>Confirmation by RNAi</b>	CT24102: wild type profile only, CT24072: Loss of G1 peak CT24092: Increase of G1 peak

**Example 53 (Category 4)**

<b>Line ID</b>	951/8
<b>Category</b>	Mitotic defects in brain: (some overcondensation, anaphase bridge, metaphase with swollen chromosome and bipolar spindle)
<b>Reversion</b>	NR
<b>Map Position</b>	73D
10	<b>Rescue ID</b> 2E8S
<b>Rescue Sequence</b>	GTATAACAAGATCCCGAGACACCGGTCAGTTGGTGCTACACGCTCTTGGAGA GCGCTGTGTTTGTTCGGTTCAGCGATTAGCGATAGTTTTGTTCGAGCCGGTTGT GTTAACTTGCTAGCTTCGGGTTTATTGTGACACTTTCCCCAAATCGATCGTTT 15 GCGAAGCGTGCATAGCGGAACATACATACATAGATAACCAGCGTGTCTGGGT GTTCATGAAAAAGAGTGCGTGATATGGGATTTCGATATGGCAACACGCTTTATG GATATACTAAAGCTGACCTTTAAGTGAGTTTTCCAGTCAGTGTCCGCTTCTTG CTCTTGCGGAGCGTTAAACGGTTTTCTGTGTTTTGAGGTCTCGCGTCTTGGTTT TGCAACAGCTTCTGCCAGCATGCACACATACGTGTGCACTGGGAAAAATAGTG 20 TTGCAGAAGTGCTTGATTATAAAATATTACAAAAAATGTGATGAAACACTTTT TATTTTCTTCAAAAAATCAAGAATAAATTAACACTATCCTGCTCTTAAACAT GGAGATTAATTCAATTTTAATTAAAAAATAATTTTTTTTACAATTTATGATTTA TGAATTTATGCACTCCTTGAACTATTAAGACTCAACAGTGA
25	<b>Genomic hit, Accession No.</b> CSC:AC015272
<b>Associated ORF</b>	Genscan ORF1 predicted sequences >23:03:05 GENSCAN_predicted_peptide_1 602_aaMGFDMATRFMDILKLTFKPFKTN 30 YTEEKYFNDKLRSSKNIERRYILDVGFGRGPTAVTYNPIWVISFKYEQRKLSTAIYSV IKTKSGPVVRGVKRNTIWGGSYFSFEKIPFAKPPVGDRLRFKAPEAVEPWDQELDCTS PADKPLQTHMFFRKYAGSEDCLYLNVIYVKDLQPDKLRPVMVWIYGGGYQVGEA SRGLDVVIVTVAYRLGALGFLSLDDPQLNVPGNAGLKDQIMALRWVQQNIEAFG GDSNNITLFGESAGGASTHFLALSPQTEGLIHKAIVMMSGSVLCPWTQPPRNNWAY 35 RLAQKLGYTGDNDKKAIFEFLRSMMSGGEIVKATATVLSNDEKHHRLFAFGPVVE PYTTEHTVVAKQPHELMQNSWSHRIPMMFGGTSFEGLLFYPEVSRPATLDEVGN CKNLLPSDLGLNLDPKLRENYGLQLKKA YFGDEPCNQANMMKFLELC SYREFW HPIYRAALNRVRQSSAPTYLYRFDHDSKLCNAIRIVLCGHQMRGVCHGDDL CYIF HSMLSHQSAPDSPEHKVITGMVDVWTSFAAHGDPNCESIKSLKFAPIENVTFKFC 40 LNIGDQFEVMALPELQKIEPVWNSFYAPNKL  >23:03:05 GENSCAN_predicted_CDS_1 1809_bp atgggattcgatatggcaacacgcttatggatataactaaagctgaccttaagccatttaaacgaactacactgaagaaaagtattt caatgacaaaactcagatcttgaaaaatattgaaaggcgttatcttgatgttggttcgcggacccacagcagtcacgtacaat 45 ccaatctgggtaataagcttcaagtacgagcagcgcaaatgtcaacagcaatatattccgtcataaagacgaaatcaggtcctgtg cggggagtggaagagaacacaatctggggaggaagctacttcagtttcgagaagatacccttcgaaagcctccggtgggagat

165

ctgcgcttcaaggccccggaagcagtgaggccatgggatcaggaattggattgcacttcgccggcagacaagccccctcagaca  
 cacatgttttcagaaaatacgcgggctcagaggactgcctctacttaaatgtgtatgtcaaagatctgcagccggataaactgcgtc  
 ccgtgatgggttgatctacggaggaggctatcaagttggcgaagcttctcaggattggatgtggatcatagtcaccgttgcctatcg  
 actgggtgccttgggcttctcagcctggatgatccccaactaaacgttcccggaaatgcaggtctcaaggatcaaatcatggccc  
 5 tgcgatgggtgcaaaaaacatcgaagcattcggcggtgattccaacaattacactctttggcgaaagtgcggcgaggcctc  
 gaccacttccttgcactaagtcaccaaaactgaaggtcttatccaaaagctatcggtatgtcgggcagtggtttgtgccctggacg  
 caaccaccgagaaataattgggcttataggctggcccaaaaattgggatacaccggtgacaataaggacaaggcgatctttgagt  
 ttctgcgatcaatgagtggggggagattgtcaaggccaccgcaacagttctcagcaacgatgaaaagcatcatcggtatctttc  
 gccttcggacctgtcgtagaaccatatactaccgagcacactgtggtcgttaacaaccgcatgaactgatgcagaatagctgga  
 10 gtcacaggataccatgatgtttggaggcacgagcttcgagggttctattctatccagaggttcaaggcgccagcaaccctc  
 gatgaggtgggtaactgcaagaatctgctaccgagcgtctcggcttaacctagatccaaactgcgtgagaactacggcttgca  
 actgaagaaggcgtatttcggcgacgaaccctgtaaccaggcaaacatgatgaagtctcagctatgctcatatcgagagttctg  
 gcacctatatacagggcagcttgaaccgtgtccggcaatccagcgacccacgtatctgtatcgattcgatcacgattccaaact  
 gtgcaacgccattaggattgtactttgcggccatcagatgcgaggtgtttgtcatggtgacgatctgtctatattttccacagcatgtt  
 15 gtcgcatcaatccgctcccgattctccggaacacaaggtataaccggaatggtcgacgtttggacgagtttcgagcccacgga  
 gatcccaactgcgaaagtataaaatcactcaagttgcacccatcgaaaacgtaaccaacttaagtgtctcaatattggggatcagt  
 ttgaagtcatggcgcttcagaattgcagaaaatcgaacctgtgtggaatagttttacgccccaaacaaactgtag

**Drosophila Gene Hit** TBLASTN with ORF1: alpha esterase (aE10) gene (U51054)  
 20 **Human Homologue** TBLASTN with ORF1 and BLASTX with U51054: bile salt-  
 dependent lipase (S79774)

**Annotated Drosophila genome genomic segment** AE003671  
**Annotated Drosophila genome Complete gene candidate** CG1131 - alpha esterase 10  
 25 **Human homologue of Complete gene candidate** 4e-48 4557239  
 ref|NP\_000656.1|pACHE|  
 acetylcholinesterase (YT  
 blood group) precursor  
 30 >gi|113037|s

35 **Putative function** alpha esterase  
**Confirmation by RNAi** Only wild type profiles observed

**CATEGORY 5: SMALL IMAGINAL DISCS (BLOCK TO PROLIFERATION)****Example 54 (Category 5)**

<b>Line ID</b>	113/20
<b>Category</b>	2nd chromosome, small imaginal discs
<b>Reversion</b>	R
<b>Map Position</b>	50D/E
<b>Rescue ID</b>	EcoR1
<b>Rescue Sequence 1</b>	CTGAGGCNCTTTGCCAATATGTGTATATTGGGCGGGGNACATGCGTNAATCGG TTAAAGCCGCTACTTACATTCTGTTCTTTGCATCTCCCCATCCACAGCTATAA AGCAAGATGAGCTACGCCGCTGATGTGCTGAACTCGGCCCATTGGGAGCTCC ATGGTGGTGGCGACGCCGAGTTGCGTCGTCCATTCGATCCCACGGNCCATGAT TTGGATGCATCCTTCCGCCTTACACGCTTCGCANATCTAAAGGGGCGCGGCTG CAAAGTGCCCGCAAGGAAGTNGCTCCCCACCT
<b>Rescue ID</b>	BamH1
<b>Rescue Sequence 2</b>	CCACCTGGTACCACAGCGCTCANACGTGTATGTACACGGATTTTCTGCCGCGT GTGTGTAGCGCGGCCCGTGATTGGCTGCAGTCGCGATGGCGGCTAAAACGGG CGAAGTCAGTATTTCTCCCTGTCGACGANGCGAGCAACGTGAACAATGCCAC TCATTTCAATTGCAAAATGCCAAAAAGTGCGCGCTTTGAATTGGCCATTTGGT TCGTTGCGTTCGTTTGTCTTTTGGTACTTACGTTTGCTTGTGCGATTGTACAAA GATAATTGTAGAGTAACGTTAGCAAATTATATTTATTTTGCGCCTGGTTTTTGC TTTTCCAACGANCGAGATGTCACAACAGGGTTGTATTANCGTGTGCGGCTGAT TCGATATTTGGGATGCCGATTGTCTGAAGCGANGGTTCAACGGGGCTGCCAAC TCCCCGAAAATCTATCNATGGTATTGTGCGCCAAGGGTAAAATAAAATAAAAA TATGTTAAAACCGCGGAATAAATGGGGGAACCGAAGTGGAAGTGTGGTTCA CAGTGCTCTGACTTTCGGGAGCAGTTAATATAGTTGGCATTAAATTCAATTAGA GCTCCAAAGTGCTGGTCAAAAGAACGCACAAGAACGGGCCATGAAAAACCT GTTGCGCCAGCAGAACGAAAAGTAAAAATTAGAAGAAACCAT
<b>Genomic hit, Accession No.</b>	CSC:AC017131
<b><i>Drosophila</i> Gene Hit</b>	rescue sequence: selenophosphate synthetase (ptuf1) (U91994)
<b>Human Homologue</b>	BLASTX with U91994: SELENIDE, WATER DIKINASE 1 (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) (P49903)
<b><i>Drosophila</i> EST</b>	LD46437 (AI514756 similar by BLASTN to U91994 selenophosphate synthetase (ptuf1) gene)

**Annotated *Drosophila* genome Complete gene candidate** CG8553 selD selenophosphate synthetase  
**Human homologue of Complete gene candidate** 1711372 P49903  
SELD\_HUMAN  
5 SELENIDE, WATER  
DIKINASE  
(SELENOPHOSPHATE  
SYNTHETASE (1e-159 )

10 **Putative function** selenophosphate synthetase

**Confirmation by RNAi** Only wild type profiles were observed

**Example 55 (Category 5)**

5	<b>Line ID</b>	121/1
	<b>Category</b>	2nd chromosome, small imaginal discs
	<b>Reversion</b>	NR
	<b>Map Position</b>	60B
	<b>Rescue ID</b>	BamH1
10	<b>Rescue Sequence</b>	
	TCCTGTGCACTCATATTGATTTGCCTTGTCAGTGGCTAAAGAAATATTAAATG	
	TTTGTTATTTCTGTTGCTAGCGCTCCGACAGTCTGGCAGCACTGCTCGCTGTCG	
	ATAGTTCAACTGAGTTGCTGTTTCATCGAACAGAGCTGCCAACTCTATTTTGT	
	AGCTGGCCAGCCAGGATTGCCAGAGTAAGGCCCTCAAATCAGCTGTTTTGTGT	
15	TTTGATTTTATTTTGAAAGTCCTAGTTTAAAATTATGCTTCTCCGACAGATCA	
	GCACAAATAATACTAATAAGCTCACAATGCTAAGGTTGTGCCTTCCAACCTCG	
	AGCTGGATATGTGCGTAAGTAAGGACTTTACGTCTATAAACTTGTTATGTAA	
	AGTAAATGTTTGCCTATTGCGCAATTTCTCCAACGAAAAACCCAGAAAACCNA	
	AACCCCTTNAAANTTTGGAATATNCCCAATGAATGCAGCACCCGTGAAATCC	
20	GTAATGCCTTTGTCCAGCTCTCCAAATTGGTAAGTAACTCCAAGATCCAAAGG	
	AGCCTCCTAAACCCTGCCCTTTCCACAGTACCACCCAGATGTTAAGAGCAATG	
	CTGCGTGTCCGGAGCGCACAGCCCGATTGTTTCAGATCTCCGAGGCGTACAAG	
	AACCTGATAAAGCCGGAACGGAAGGAAAAA	
25	<b>Genomic hit, Accession No.</b>	CSC:AC020499
	<b>Drosophila Gene Hit</b>	rescue sequence: DnaJ60 gene for dnaJ-like protein (Y11900)
	<b>Annotated Drosophila genome genomic segment</b>	AE003463
	<b>Annotated Drosophila genome Complete gene candidate</b>	CG12240 – DnaJ60
30		CG13570 – spaghetti ser/thr phosphatase
	<b>Human homologue of Complete gene candidate</b>	CG12240- 4827026 ref NP_005138.1 pTID1  tumorous imaginal discs (Drosophila) homolog >gi 3372677 (AF061749) 7e- 08
35		
40		CG1116- 2495728 HYPOTHETICAL PROTEIN KIAA0258(aa)
45	<b>Putative function</b>	CG12240 : Chaperone involved in protein folding CG13570 : serine/threonine phosphatase

**Confirmation by RNAi**

CG12240: Marked reduction in G1 and G2/M peaks  
indicating fewer cycling cells

CG13570: Marked increase in G1 peak

**Example 56 (Category 5)**

**Line ID** 127/2  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** NR  
**Map Position** 57F

**Rescue ID** EcoR1

**Rescue Sequence 1**

10 GCCGGTGGGCCCACACTTGTNCGCCCGCGCATCGGCTGTCTGTGGGAGTGCGA  
NCGAGTCAGATAGTAGATCCGATGCGCTCTCCAGATACTTTTTGAACACTGAA  
GAAAACGCGCAGTTGTGGGTGAATTCAGCATCATCAGATTGAATCACACACA  
ATCCTAGTCGCCTCACGCGAAGAGAACTATGTCATGATCAGATATCGGTGTAT  
GCATTCTATATTATGTA CTTCGAAATATGTAATTTATTAAGTTTTCGCTATACT  
15 TTTCAATCAAATTGGCAAAAACCAATTCAAAGGTTTTCAATATTTTCGAAAAG  
CATTTTAGGCTTTCTATGTAACGTATGTTTTTCAAACAAAATATTAGTTTTTGA  
AACTTTATTATCGGATAAACAAATGTAAGCCAAATNACAACGTTNTATGATAC  
TCCCAAAGATCCGCNCTNTTAAAGTGGCCTAAAAATAGCTGACGCATTAANCC  
ATAGGCGCTTCGCTTCTCAAGATAAACCTGGCGTGCTCAACTCAAGAAACAA  
20 ATATGTGGTTATATACATATATACATATATGGGGCATATAACCGATGTGTGAC  
GTGACATTGGCTCGTTCTATTACATACTTAAACACTAAATGCAAACCTATCA  
AAAACCNACTACACTAAGCGAAAAACGGCAGANATAGTTAAGGAAAGTGGTC  
CA

25 **Rescue ID** BamH1

**Rescue Sequence 2**

CTTCTTTTCTCAAAAAACGTCGCTCGNGTCCCNCAATCGTTTTACAACTTCGC  
TCGGAACGGACGTGTGCGCGCTCTGAAAGGAAAAAGTGAAAAAGTGTGTGAC  
AAAGTGCAAATAAGCCACAACGCGCATGTGAGAAATCAAATTTAATTGAGAA  
30 GCATCAAAAATTGTATACATATCGAGCGTATCCACATCGCTGTATGTGTGAGT  
GTGCCAGTGCTAGTGTGGTTTTCCCTTTTCGCCGTGGAAAATATGAAAACCTGA  
ATGAAAAACTGAATCGCAGTCAGCCAGAGCCGAATTGGAAAAGAGTAACTCG  
CATTGGGGACACGAAGAGGTGTCTCGAAAAAGGTAAAATCTTTTACACAGAA  
ACGACGCCAGAAAGCGATTAGCGATTTNTGACTATGTGTGAGTGTGTAATTC  
35 GGTCTACGGCTGTGTGTCTGCATTTTATTTAACNTTTTGTTTCCNGTTNGNTC  
CACNGTAAAAATAGCTAAAAAAAAGGGCAAGTACTCTTGCGCGCTCTCCC  
TCTCTCTTTGTTGGTCGTGACTGCGACGTCACCGTTCACGTAGAATCGTTTTCA  
AGTGGCGTTTCTTTCTTTCTTTTAAATGTGCTGCTTCTTGCTTCTGCCTCTTCTTC  
TTGCCCTTTGGCTATCTGCTTTGTTTTGAAATACGTCCATGTTATTCCAGTGTCTG  
40 TGCCAAATGTGTGCGANATGATCTCTACTT

**Genomic hit, Accession No.** AC009732

**Associated ORF**

45 Genscan ORF1 predicted sequence  
>/tmp/aaaaafrla|GENSCAN\_predicted\_peptide\_2|456\_aa

MQTKGPITDADCIRGMACRALAGLARSDRVRQIVSKLPLFASGQLQTLMRDPILQ  
 EKRAEHVIFQKYALELLERVSGKTKPLNNPLDPSLSNMHKANVIAQTRIQYNKQQ  
 LYQLIFEHLESNGLSQTAQMLQREVGLPLQTPTRSFHQSPFDYKSLPSGSSSLSRN  
 RLRSRMQDVNAAIMGNGLNRSFGEDSSPAGAGGSNAGDGVSIPIFSSLNTTQTP  
 5 IKIRRTDRSSVSRSIQKQAMEPGGMSVGLAEDGQLHPKRITLNTIVTEYLTNQHSL  
 CNNPVTTCPQFDLYEPHKCPDPKPSRLLSSNYNLTSRHARTQAGFNTSRFDRRYV  
 HTHFSPWRSIRSADYEDLEFTCCDLGKYIIVGTQQGDGRVFNMNNDGVEQFFSNC  
 HNFSDAIAKANRAGDLVITSSFWRTPTSILWSIADDEFKLKLRLPDVTYCEFSQTV  
 QDRLLGTQNEVY

10

>/tmp/aaaaafrla|GENSCAN\_predicted\_CDS\_2|1371\_bp  
 atcgacaccaaggaccattacggatcgggactgtatactggaatggcctgtagggccttggcgggacttgctcgctccgatc  
 gggtcaggcagatcgctcagcaagcttccactcttggcagcggacaactccagacgctgatcgggatccatactccaggaga  
 agcgcgcggaacatgtaattcttcaaaagtagcattggagttgctagaacgagtgctgggtaagacgaaaccgctaaataatcc  
 15 ttggatccatcgctgtccaacatgcacaaggccaatgtaatgcccagacacgcatccagtataacaagcagcagctgtatcagc  
 ttatctcgagcacttggaagcaacggctctctccagacagccaaatgctgcaacgggaggtgggtcttccgctacagactcc  
 cactacgcgcagtttcatcaatcacctttcactacaaaagcttccagtggttagtagctcgctgtctagaaatcgctgcgaagc  
 cgcatgcaagatgtgaacgcagcgataatgggcaatggagacttaaacagaagtttggtaggactcctcgccggcaggagcc  
 ggtgtagcaatcgccggagatggagtcagcataccaaatttagctcccttaacacaacgcagacgcccataaaaataaggagg  
 20 acggatagaagttcagttagccgctctatccagaagcaggcaatggagcctggtggcatgtcagttggtcttccgaagatggtca  
 actgcatcccaagaggatcacctaaataccatcgtaacggaatacctcaccaaccagcactcgctgtgcaataatccggtgaca  
 acctgcccgcagtttgattgtacgagccgcacaagtgccagatccgaagccagccgattgctaagctcgaactacaacctga  
 ctatgctggcatgctcgaaccaagccggatttaataaccagtcgcttgaccgctgctatgtgcacacgcacttttaccatggcgta  
 gcattcgatcgccgggactacgaggacctagagttcacctgttgcatgttggtgggtaatacatcattgtgggcacgcagcagg  
 25 cgacggacgagtggtcaacatgaacgatggcgtggagcagttcttccaactgtcacaactttagcgttgatgtattaaaggtaat  
 agagccggagacttggtcatcacatctagcttctggcgacacccaccagcattctatggtctattcgggacgatgagttcaagcta  
 aagttgcgacttcccgatgtcacgtactgtgagttcagtcacaacgggtgcaggatcggttggtggcaccagaatgaggtatactaa

30

corresponds to CG10082

**Drosophila EST** several including SD04293 (AI532704)

**Annotated Drosophila genome genomic segment** AE003454

35

**Annotated Drosophila genome Complete gene candidate** CG10082 – novel protein with  
 homology to enhancer Pi  
 uptake

40

**Human homologue of Complete gene candidate** 1665793 dbj|BAA13393|  
 (D87452) Similar to  
 S.cerevisiae YD9335.03c  
 protein (S54640) [Homo  
 sapiens] (2e-43)

45

**Putative function** Putative phosphatase or enhancer of Pi uptake protein

**Confirmation by RNAi** Reduced G1 and G2/M peaks indicating fewer cycling cells

**Example 57 (Category 5)**

**Line ID** 131/8  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** R  
**Map Position** 60A

**Rescue ID** BamH1

**Rescue Sequence 1**

10 CACGATTGCNNGGCCCATCGAAGTGTGGGTCTATCGATACTCGTGGGTAAATAA  
ACAAGTTCTGAACTGCGATTTTCGGGGGTTTGAGGGGTCAATTGTCCCCTGTGT  
TGGAATGTGTTCTTAAATCTACACAAACACTCCCTAAGCTTATCCTAAACTTAT  
AAATATTGGTTGCTATTTAAACCCCATTTACGGTTATCCAGCACGCCCCCTGA  
ACTGTGACCCACATCCCCGATTTTAGTGACTAGTTTTATACTTATCGTGGTTGG  
15 CATTTGGTACACTACACTTTCTTATTACCTAGATCGCCGACTCCGCGCACGGT  
CGCGCTCCCGTTCCCGCTCCCGATCTCGGCTGCGACTGCGGTGCGATCCCGTT  
CCCGGTGCGGCGACCGGCGCCTCCANATCCGGATCCCTAANCGGCANCNGT  
CNTGGTGGCAATCNNGGAATGTTCCGGGGNCCNCTACNCAGTGNAATCAC  
TGGTACGTCCCACCGCNAACTCCGCCCANTGCGGTTGCCGGAACGGGTGGC  
20 ANTGCCAATGGGTGCTGCGAAGGTACCATCACAGCAATCGCTCACGGANC  
CCGAAGACTGCCTCTGCCGCCCCGGCTGGGCCACTCATACACGCTACACGGTGC  
GAAATACTACATTGATCACAATGCGCATACCACGCACTGGAATCATCCGTTGG  
GAACGC

25 **Rescue ID** EcoR1

**Rescue Sequence 2**

AATTGATTTCCGGACATATAAACAGAATCCAGAACTCATCCGGCAGCAGGCTC  
AGTCAGGCCAGTAAATCCGAAAAGAGAGTAACCAGCAGGAAAAGAGAATCC  
ACGTAAATACAGAGAAAATGGCTCTACGCGTCCAATTCGAGAACAACGACGA  
30 CATCGGCGTATTCATAAATAACCAACACATACTGCCTGGTGGCCATCGGTG  
GATCCGAGACCTTCTACAGCGCCTTCGAGGCGGAGCTGGGCGACACCATCCCC  
GTGGTGCAATGCGAATGTGGGCGGCTGCCGGATCATCGGCCGCCTCACCGTGGG  
CAACCGCAACGGCCTGCTGGTGCCCAACTCCACCACCGACGAAGAGCTGCAA  
CACCTGCGTTACANCCTGCCANAACCCCGGAAANATTTATCGTGTGGAAGAAC  
35 GCCTGTCCGCGCTGGGCAACGTTATCGCCTGCAATGATTATGTGGCCCTGGTG  
CACCCGGATCTGGACAAGGAGACCGAGGAGATCATCGCGGACGTGCTCAAAG  
TANANGTCTTCCGCCAGACCATTGCCGACAACCTCACTGGTGGGCTCTTACGCC  
GTGCTGAGCAACCAGGGGGGCATGGTGCATCCCAAGACNAGCATTACAGGAAC  
AGGACAACTGTCGTCCCTGCTGCAGGTTCC

40

**Genomic hit, Accession No.** CSC:AC020517

**Associated ORF**

45 Genscan ORF1 predicted sequences >22:13:05|GENSCAN\_predicted\_peptide\_4|357\_aa  
MALRVQFENDDIGVFTKLNTYCLVAIGGSETFYSAFEAELGDTIPVVHANVGG  
CRIIGRLTVGNRNGLLVPNSTTDEELQHLRNSLPDAVKIYRVEERLSALGNVIACN

DYVALVHPDLDKETEEIADVLKVEVFRQTIADNSLVGSYAVLSNQGGMVHPKTS  
 IQDQDELSSLLQVPLVAGTVNRGSEVLAAGMVVNDWLSFVGMNTTATEISVIESV  
 FKLNQAPATVTTKLRAALIEDISRSRVAGGGGGGGGGSSGGNSSSGPSTSRRTT  
 RNNAAATAADRPKINEADLEGKSPEEVEMLKTMGFCTFDTTKNRKVEGNDVGEV  
 5 HVILKRKYRQYMNRRKGGFNRPLDFVA

>22:13:05|GENSCAN\_predicted\_CDS\_4|1074\_bp

atggctctacgcgtccaattcgagaacaacgacgacatcggcgtcttactaaactaaccaacacatactgcctgggtggccatcgg  
 tggatccgagaccttctacagcgcttcgagggcgagctggggcgacaccatcccgggtggtgcatgcgaatgtggcggtgcc  
 10 ggatcatcggccgcctcaccgtgggcaaccgcaacggcctgtggtgcccactccaccaccgacgaggagctgcaacacct  
 gcgtaacagcctgccagacggcgtgaagatttatcgtgtggaggagcgctgtccgcgtgggcaacgttatcgctgcaatgat  
 tatgtggcctggtgcacccgcatctggacaaggagaccgaggagatcatcgaggacgtgctcaaagtagaggtcttccgccag  
 accattgccgacaactcactggtgggtcttacgccgtgtgagcaaccaggcgccatggtgcatcccaagacgagcattcag  
 gaccaggacgaactgtcgtccctgtcgtcaggttccctcgtggcggaacagtgaaccggggcagcgaagtactcgccgccg  
 15 gcatggtcgtcaacgactggtctcctcgtgggcatgaacaccacggccacagagatcctcgtgatcgagagcgtcttcaagctt  
 aaccaggcacagcccggccacagtgcgacccaagctgctgctggccctcatcgaggacatcgcgggtcgaggggtcgccgga  
 ggaggaggaggaggaggcgccggcggaagcagcgccgggcaacagcagctccggaccatcgacgtcgcgaaggacgacg  
 aggaacaatcgccggccacagctgccgaccggcccaagatcaacgaggcgacctggagggtaaatcgccggaagaggt  
 cgagatgctgaagacaatgggattctgcacgttcgacaccaccaagaacagggaaggtcgagggcaacgatgtcggagaaggtc  
 20 atgtaatcctcaagcgaaagtaccgccagtlacatgaatcgcaagggtggcttcaaccggccgctcgatttcgtggcatag

**Drosophila Gene Hit** rescue sequence and TBLASTN with ORF1: b(2)gcn  
 (EUKARYOTIC TRANSLATION INITIATION FACTOR 6  
 )(X97641)

25 **Human Homologue** BLASTX with X97641: integrin beta 4 binding protein (HUMAN  
 EUKARYOTIC TRANSLATION INITIATION FACTOR 6)  
 (NP\_002203.1)

**Drosophila EST** GH08760 (AI109537 similar by BLASTN to X97641  
 "D.melanogaster b(2)gcn gene." )

30

**Annotated Drosophila genome genomic segment** AE003462  
**Annotated Drosophila genome Complete gene candidate** CG17611 – bcgn benign  
 gonadal neoplasia homology  
 to Eif6 translation factor

35

**Human homologue of Complete gene candidate** 6016331 EUKARYOTIC  
 TRANSLATION  
 INITIATION FACTOR 6  
 (EIF-6)(aa) and 4504771  
 40 |ref|NP\_002203.1|pITGB4BP|  
 integrin beta 4 binding  
 protein(aa)

45

**Putative function** eukaryotic translation initiation factor 6 (eif-6)(aa)

**Confirmation by RNAi** Slightly reduced G1 and increased G2/M indicating block in  
 G2/M

**Example 58 (Category 5)**

	<b>Line ID</b>	135/25
	<b>Category</b>	2nd chromosome, small imaginal discs
5	<b>Reversion</b>	NR
	<b>Map Position</b>	24A
	<b>Rescue ID</b>	EcoR1
	<b>Rescue Sequence</b>	
10	ATAACATGGGCNCTGGTTTTTAAAGTNAAGCTCTANTNATTGGCCCCCATTCTTA	
	NNCTCTCTCGCTCTCTTCTCGCTCTTTCGCCTGCTCTCTCGCCTGATTATTCTGC	
	TTGGTCGGCTGATGGTTTTTNGTTTTNATCTGGTGTATTTTCTGCGTAGTTTATG	
	ACAAACCGGCTGGTTCCTTGTTGTTATTGCCGTATTCTAATATATTTCCCTATTG	
	TTCTTATTTTTGTTGCAGCCTGCACACCTCGGAGGTTCTAGATGATAAGGGGTG	
15	TAGCGATGGTGGGGGGCTGTCTTGANGGGCTTCTCGCCTTGAGCTCTTGTTTAT	
	CTTTGGTCATTTGTTATTGTTTAATGCACGGCAATATTATTGGTAAACAAGTTA	
	GCCAACAGCACTAAACGCCAATCGCATTCTTTTCTAAAAACCAAGTCTATTGT	
	CGATCTTGCTAGGGAAATGATGATGACTCAGGTGCAATTGGGATCTTATCTAT	
	GGCTGTCTGGGAATCAAGAAGTGTTCCCGCAGAATTCGTGAANTACTGCCGCT	
20	CTCTCCATGGGGCCATTATTTGCACTCGTTTTNCGCGAAATACCATNAATTAGC	
	ATAAAGACACGTCGCCGGCAATCGTGACGTAGGCTATNAATGCCTTCTATGCA	
	TGTGCNAACTCGCGGAAGCATAGCAATTTGAAGGAACAATATTTTCANTGCAG	
	GTTTTAATGGGCTAAAAAA	
25	<b>Genomic hit, Accession No.</b> CSC:AC014199	
	<b>Associated ORF</b>	
	Genscan ORF1 predicted sequences >20:54:54 GENSCAN_predicted_peptide_3 117_aa	
	MSASPTARQAITQVMPMITRKVVISDPIQMPEVYSSTPGGTLYSTTPGGTKLIYER	
30	AFMKNLRGSPLSQTPPSNVPSCLLRGTPRTPFRKCVVPVTELIKQTKSLKIEDQEQF	
	QLDL	
	>20:54:54 GENSCAN_predicted_CDS_3 354_bp	
	atgtccgcttcaccaccgcccgtcaagccatcaccagggtatgccatgatcaccaggaagggtgtcatctcggatccgatcca	
35	gatgcccgaggtgtactcctcgacgcccggcggaacccttactccaccactcctggaggcaccaaacttatctacgagcgggc	
	tttcatgaagaatcctcggtggtccccattgagccaaactcgcgctccaacgtgccagttgcttgcaggggaactccgcgta	
	ctccctccgcaagtgcgtgcccgtccccacggaactgatcaagcagaccaagtcgctgaagattgaggaccaggaacagttcc	
	aactggatctgtag	
40		
	<b>Drosophila Gene Hit</b>	TBLASTN with ORF1: BcDNA.HL08053 mRNA (AF132557 )
	<b>Human Homologue</b>	TBLASTN with ORF1 and BLASTX with AF132557: eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2) (L36056)
45	<b>Annotated Drosophila genome genomic segment</b> AE003579	

**Annotated *Drosophila* genome Complete gene candidate** CG8846 - phas1 translation initiation factor 4E binding protein 2

**Human homologue of Complete gene candidate** CG8846 - 4758260  
ref[NP\_004087.1|pEIF4EBP2|  
eukaryotic translation initiation factor 4E binding protein 2 (4e-16)

**Putative function** EIF4E translation factor binding protein

**Confirmation by RNAi** Slight reduction in G1 and G2/M indicating fewer cycling cells

**Example 59 (Category 5)**

**Line ID** 141/12  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** R  
**Map Position** 21A/B

**Rescue ID** BamHI

**Rescue Sequence**

10 GGCTCTTTTCCAAANAGGCAGTTTCTTGNCCCATTCTTGGATTGCTTTGTAGT  
 GAACTNAATCGTTTTTGTGGTTCCTCTGTCTCCAGTCTTGTGAAAATTTCTGTG  
 ATAATAATGCCTGGATAAATANTTAAGCATTTGGAAAACGGGGGAAAAAGGG  
 CTAAGTTGTGTGAAGGAAACAATTGAAGTGACCCTTTGTNTATAAACATTCCA  
 CGACGTGTTTCGAAAACAAACAAAGATATGCGGAAACAAAGTGTTAATAAAA  
 15 GAGCNAAAAATAGAGAGAGAGAGTGTCTCGGATAAGCGGTTGAGCGAGATAGAG  
 AAAATTGTTGATTAAAAATGTGTGTCNAAATAAAACATCAAGCCGCTTGAACGA  
 ACAGTCAGTTAGTTGCTTCTGATAATAACCATGGGAAGCGGCNCGTGTGCTTC  
 GCTCCTCGTTACTTATAAAATATTTAAACGTTTGCATTCTTCNTATTTCCGAAT  
 TTTTGCNCCCCTGAANCAACTTNGTTAAACTGCAAATAGCAATGCAAACAAAC  
 20 GAATAGAAACTGAAATCGACAACNACATGTGAAATTCACAAATCAAATCGCA  
 ATTGTCATCCCAAAGATATAGAACAAGCTATAGGGAAGATANAGAATGTAAG  
 TGCCAAACTAAAATAAACAAACAAGAATAACATTTCCACAGGTGTTTTGCATT  
 TCAAATGCATATTTCCGTGGCGGNTACAAATCTTTTCAAACCG

25 **Genomic hit, Accession No.** CSC:AC017815

**Associated ORF**

Genscan ORF1 Predicted sequences >17:48:30|GENSCAN\_predicted\_peptide\_2|554\_aa  
 MSNKKMFNRRTTSVSPGQLHYYHTDFYYSMPDLHKTRKMHGVKRVLVFCLMIVIL  
 30 PAILIIMPLHLRKTVFADVYPMAESDIIIRAGISSIFCSKHTLRMNSNFNAFQLRNK  
 PEIATNRKHIRLKKSMITLPDDTLEYWGFLLKGAKVRVKFCSRVDGSRILIIHGHR  
 ELNLCGLTDHNKNKLGANYAKGHEQVQVFFEDNVEITEEKGNQDVLMEHENHG  
 GEDLTEDIPQPQVNIPVKQNNIQPKLIRKKLKGTHHGEHDMHAITDLQGSHTT  
 EHILNHHDHSSNSPAHHHNSTAHHREHSSNITNEETS RNHIRNEDEDPDQNSSKTH  
 35 YSAESPPHRERLKRHN RV AHRNQKRQDLYDTLYKRSKRENVYDRKTIHGGNAIN  
 FTETDESNSVSSFETGLFQCFNGMILLQEFFRPKNECSNPHIMDTSPNKSSMVVHN  
 VIEDGYYYYIFYSDNDHVQNEIHAIFDIYKPTYQYSNMSESQSCLNTTNCTFNISFL  
 SDEIVVVEVPTRDIEHEEDDITNLISTCHPRSEIYAIFPITVLVLILCCSFL  
 40 >17:48:30|GENSCAN\_predicted\_CDS\_2|1665\_bp  
 atgtccaacaaaagatgttcaacaggactacgtcagtaagtcctggacagttgcattattatcacacggatttctattactcaatgcc  
 ggatttgcataaaacccgcaaaatgcacggcgtgaaaaggggtgctggttttctgcctgatgattgtgatactgccggccattcttattc  
 attatgccgctgcatttgcgaaagacgggtgttgcgacgtcatctatcccatggcggagtcggatcattgagattcgggcaggaa  
 atctcgtcgatcttttctcgaacacacactgcgtatgaactccaattcaacgctttcaactacgtaataagccggaaattgcgac  
 45 gaatcgcaagcacattaggctgaagaagtcgatgacattgccggatgatacgttgaatactggggcttcttctgctgaaaggtgc  
 caaggtgcgagtgaaattctgctcccgctacgatggatcccgcattctgatccatggtcacaggagcttaattcttgcggtct

177

gaccgatcacaataagaataagttggcgccaattatgccaaaggtcacgaacaggtgcaggtgttcttcgaagacaatgtggag  
 atcacggaagagaaggggaaccaggatgtgctaattggagcacgagaaccacggcggagaggatttgactgaggatattccaca  
 gccgcaggtgaacatacctgtcaagcaaaacaattctatacagcctaagttaattaggaaaaaactgaaaaagggcacaattcatc  
 atggcgaacatgatatgcatgctataacagattgcaaggatcacaccatacggaacacatatgaatcacatgatcacagctcta  
 5 attctccagcacatcatcacaatagtactgcccatcatcgggagcacagttcgaatatcacaacgaagaaactagtcgtaatcaca  
 tacgaaatgaagatgaagatccagatcagaattcaagtaagaccattatagtgcggaaagtccgcctcaccgggaacgtctcaa  
 aagacacaatagggtagcccataggaatcagaagagacaggatctttacgatacgtttataaaagatcaaagaggggagaatgtc  
 tacgatagaagacgatccatggaggaaatgctataaattttacggaaacggacgagtcgaattcgggtgtccagcttgagacagg  
 actatttcagtgtttcaatggaatgatcctgtgcaggaggttcttcaggccaaaaaatgaatgctcaaatccgcacataatggacactt  
 10 cgcccaacaagagttccatggtggtgcacaacgtcatcgaggatgggtactactattatattctacagcgacaatgatcacgttc  
 aaaacgagatccacgccatattcgatattacaagccgacgtatcagtactcaaacatgagcagagtcacaaagctgtctgaatacc  
 acaaattgcacattcaacatcagtttccttcggatgagattgtggtgggtggaggtccaacacgggatggtatcgagcacgagga  
 ggacgatataaccaatctgatctccacctgtcatccgcgcagcgagatatacgccatctttccattacgggtgctggtgctgatccttt  
 15 gctgctccttctgtag

corresponds to CG9524

**Annotated *Drosophila* genome genomic segment**

AE003623

**Annotated *Drosophila* genome Complete gene candidate** CG9524 - novel His-rich  
 protein

**Human homologue of Complete gene candidate**

none

**Putative function**

No homologies which indicate function

**Confirmation by RNAi**

Reduced G1 and G2/M peaks indicating fewer cycling cells

**Example 60 (Category 5)**

	<b>Line ID</b>	146/2
	<b>Category</b>	2nd chromosome, small imaginal discs
5	<b>Reversion</b>	NR
	<b>Map Position</b>	26B
	<b>Rescue ID</b>	EcoRI
	<b>Rescue Sequence</b>	
10	TTTNATCCAAACTGAGANACTNNTGGCCCCAAAACTGAAAACTCGGACTCGGG	
	CGCGTAAGGGAGTCGGTCNTCGGGAGTCGGTCGTCTTTTGTGATCTTGAGAC	
	TGAAATTCCAATTGTTGATTTATCTCTCGGCTGCTGCGCCGCGGCTGCGCTGCT	
	GCAGCGCAGTCCCACTCCGATTTGACCAGCGACCAAGTTTATAAACTTTGAG	
	CCAAAATGCAGCGGCGCACAGTTGTTACCAAAACGTTGCACGCGTCGTGGCCC	
15	TCATCAAAACAAAAAATATAAGCGAAAATGAAAACGAAATTCGGTTA	
	ACGTCAACAGAAGCTGACAAAAGGCAGAAAAGACCGAAACAAGTTGCAGGG	
	CCAGAGTAAGCCAAGTTAAATGCGAAAGAGAAGCAAGAGNCAAGAAGAAAN	
	AATGGGCACTACATACATATATTATAGCCAGCTAATCTGTTGTGCAGTGC GTT	
	TTATCAGCCNNCGAAAAGAAAACGAAAACGAAAAGTCGGTCCAAGTTCGGAC	
20	TCAAAATCCAAACAGAAGAGACTCCATNCCATCAGAGACACGCGGATCTCAT	
	CTCGGTAATGTCTCAATAAAAGTAATCTTAACTGCCGCCGGAATGTTGGAAA	
	AAGTGAAAATTGAAGCGCTTAACGTGTTTCGAAATACGATACATGAGAAGTCC	
	CAAAAAAAAAA	
25	<b>Genomic hit, Accession No.</b>	CSC:AC019865
	<b><i>Drosophila</i> EST</b>	GH19286 (AI388389)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003481
30	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG11353 - novel with weak homology to sugar acetylase? CG7525 - tie receptor protein tyrosine kinase.
35	<b>Human homologue of Complete gene candidate</b>	CG7525- 4e-23 4557869 ref NP_000450.1 pTEK  TEK tyrosine kinase, endothelial >gi 464868 sp Q02763 TIE2_
40	<b>Putative function</b>	Sugar acetylase and receptor tyrosine kinase
	<b>Confirmation by RNAi</b>	Both gave a reduction in G1 and increase in G2/M peaks indicating arrest in G2/M

**Example 61 (Category 5)**

**Line ID** 155/13  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** R  
**Map Position** 21B

**Rescue ID** BamH1

**Rescue Sequence 1**

10 GNTTTAGTCCNCTTTTGANAGGGNCTTGGNGNCTTAAANAANNAAAAAAGGG  
 GNCCCGGCNCCCAGCAAANAGNNTAAACTTGAATGGTTTAATTCGAAAATC  
 TTTTAGAAATGTCGCCTAATACCTTATCGGTATAGAGTTCACCTCGTCTCCTAA  
 TCCATATTTTAAAGATATCAATATCTATTAACAATTTTATCGTATGATTAGAAA  
 TTCGCATTGTTTTATTATTTTCGACCTTTGGGCTTTACATCGACAGCTACTCTCTA  
 15 TCCAGACAGGAGACTGGGAGAGAGAGCACGATGCTGTCTGAAAGCATGAATG  
 ATGGATGCTGTGCCTATGTGCGATATGCACGTTGCCTGAGCTAAAACGAAACG  
 AGATTATTAATCTATCCGCAAGATTCAGATGCTGATTCCACATGAGTGAGCGA  
 GTCCGTGAGTGGATATTGCTCTCTCCGAAATGCATGCATGAGTGAGCAGGGGG  
 GCTTCAATCGCNCTNTCGATNTGCGACAGNGACATNTTTTATCTTCGACNAT  
 20 GCNCTCNCTCCCTCCCACAGAAATCTTGCGCTNGNTCTCCGANNTNGGGNTNG  
 ANGGCNCTCTTCTCTNTCCTTAAATTGGGANTTNNCTTTTTTCNAANAAGGGN  
 NAGA

**Rescue ID** EcoR1

**Rescue Sequence 2**

25 AATCNTTTTNTCCATTNGGCGNCTTNCTCAAAACATATTCACATTTGGNCCCAA  
 CGGCGTANGACTTNATCTCACGATTGTTTGGTTTCCTACTCTCCCGCGCTCCCT  
 CTCTTCTGAGTCTCTTTCTGGCTGATTTCGCATTCGATTTTAGCCGCTGCCATCG  
 CCGTTGTTTTGCCTACCTATGTGTGTGTGTGAGGAGTGTGTCTTGATTTTCAGT  
 30 CCGCAATGCGCTCCGCTCATTATTTGTTTGANCGCCGCGGTGTAAAGTTGTAA  
 AAAGTCCAAGTGCTCGTGGAACCTCGATGCAAGACGGGGAAAACGAAACGCG  
 ATAAATCGTGAGAAAAGAGAGTGCCTAAAGGAAGAGGGAGTGATAATCAN  
 ACGAAATGGAATAATGTNTTTGCAGAGGCNACAACAACAATGCAAATAGTTG  
 TCATTGAGGCGCAATGAATGATAATTAGTGCTTANTTGAAATCATAATCNTGA  
 35 AGAAAGCGTAAAGCTCGATTNTGGCAATNTATTCTTGATTACCANTGAGTCTG  
 TGATATTGCCGTGTGTNCCGAAAATGGANGTTATNAAACCCATGGACTTCAGC  
 ACCTTCTCCGCGTTCTGCGAACATCTTAACAAATCTCCACAAAATTGCAGCAA  
 CAACTGCANCGACGGTACCGCCAACTATAANCAATGGAAAANGCATTATTTG  
 GAGGTAANAGCNAAAAATACCAATNTTCCAATGCGAAATTGCNAGCNTGG

**Genomic hit, Accession No.** AC004274

**Annotated *Drosophila* genome genomic segment** AE003590  
**Annotated *Drosophila* genome Complete gene candidate** CG13693 - novel

**Human homologue of Complete gene candidate** 6e-05 4507659 translocated

promoter region (to activated  
MET oncogene)  
>gi|1730009|sp|P12270|TPR\_  
HUMAN POOR MATCH

5

**Putative function**      No homologies to indicate function

**Confirmation by RNAi**      Only wild type profiles observed

**Example 62 (Category 5)**

**Line ID** 162/24  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** R  
**Map Position** 55C

**Rescue ID** EcoR1

**Rescue Sequence 1**

10 TTTTNTTTTTCANGGNTCTTTGCNCATAAAAANACACGNGCCCTCCTGTCCATTTCAC  
ATTTTACTTGGAGTCGGTAACGTTGAGTTCCGCGTCCGTGCGTTCTGCCTTCCA  
ATACAAAGTCTGGTGTGAATCTACCAAGCATTCCAGTGNGAAAATCAACTCAC  
ATTGCTCGGTGATCCNTGCGGCGGTATNATCGCACCCCGGAATTGCATAAGTTG  
CGNGAGCGGAAAGAGAGTGCACGGATTTCNCGTTATCNAAGGGCCGCGCANC  
15 NGTGGGGCGGCGACGGNAGAGCACGCAGAANAANAATANANTGNNGTGGCG  
AATTNAAAAATANNATNAAAGAAAATTTCGGGCCGCTAATTTTTCTTCAAATTT  
GTGTGCGGTTCGGCGAAAAACAACGTGTTTTTCNATGGTTGATAATACACACGG  
ACGGNNCACTCGCGCTCACCCACATAGTCACNAAAGTCGGCGACGTTCGACGA  
CCNCACNCTCACATANGGACNTTTAATCCCGTNCATNCGTGTAGCGTNCNTA  
20 TTTAACCNTNTCTGTCCATCGGAACGCNCGCNTTCTCGCCTTCNTTCTNCTTTA  
CTTTAATTTCTTATTNNAAAGGGGNAGNCCNATCTTTTNCCTNTCNNTGCCNT  
TTAANNTCATCCACANCCTCNCTTTNTCNTTCTCCNCCTTNTNTTCTTTTNTC  
TTNCTTNTGNCCTTGCCCTCGTTCTTTCTCTTCNTCTCCTTNCCTTCTCCTCCTTT  
TTTCTCCTTCCCCC

25 **Rescue ID** BamH1

**Rescue Sequence 2**

AAGNCNCCTTGGCCGNNTTNAACGGNAANTAANCCGGGNCCNCGGGNCNCGA  
TAATCAGGTCNANCCTTGTGCCTACCACCACCAAATTGAAAAAGAGCNAAGA  
30 TTCTCTAAGGCAAAAACTCCCCAATCTGTGGAATTTCCGGAAGCGAGAGCAC  
ATTCAAAGCTACCAGTTATCAGCGAGCAGCATGTCTAAGCTCAGGAACCTGTT  
GCCACAATCTTTGGCGGGAAGGAGGCACAGAATCCGACACCCGTTCGAGGGA  
CGCCTGGAATAGGACGCAGCTCCCGTGGACGACAACGAACCNGATTACTACT  
ACTGCGGAGCCATGGCGCTGCCCTCCACCGCTGGCACGCCCACAGCCTCCTCG  
35 GATCTGACCGAATCCGTGCTGCGCGAGCTCAGCGACCCAACTACAATTCAAT  
GGATGTGGTGCTTTTCNNCCTNTTTTCCGGGCACTCTCAGTAACGTCCAGACAA  
ACAACACCATGAACGTTACNGCGCCCAGCAACAGGTGGTCATGAACTTCTCG  
AATGCCAATAATCTGCACTTCGGCTCCGTCTTCAACTTCAACCAAACTTGAG  
CGCCTGCNGCTCNCGAANGGGTTTACCNGTTCGCANAAGAATCGGTTCGCCTC  
40 TCCANACNGT

**Genomic hit, Accession No.** CSC:AC012981

**Associated ORF**

45 Genscan ORFs: ORF2 predicted sequences  
>18:26:17|GENSCAN\_predicted\_peptide\_7|1320\_aa

MEETNNATTIEQQPIALINGQEQVANEQQPSSPTSVATPTSTTSGGTGNATPAFSY  
 DDLFPALPANTSQAQSQSGASGSTLARVTSSQKTHIVHVPCKERKSTSEKFGEGES  
 KRICQQITKETGAQIEIASRQVTVPREHFRVILGKGGQRLREIERVTATRINIPSQSD  
 ESEFITIAGTKEGIAQAEQEIRQLSAEQYKKSSDRITVPKVYHPFIVGPYSENLNKLQ  
 5 EETGARINVPPQQVQKDEIVISGEKDAVAAAKAKVEAIYKDMKKCSTVSVEVAK  
 PKHRYVIGPKGSTIAEILQLTGVSVEMPPNDSPSETITLRGPQVALGNALTVVYQK  
 SNSVKSVEINAAHWIHKYVFGRKGANMKQLEEDCPNVNVNCLDKIKLEGDPEN  
 VDRAYAYLSEIKNYEENFTFEVMTVNPSSYKHIIGKAGANVNRLKDELKVNINIE  
 EREGQNNIRIEGPKGVRQAQLELQEKIDKLENEKSKDVIIDRRLHRSIIGAKGEKI  
 10 REVKDRYRQVTTITPTQENTDIVKLRGPKEDVDKCHKDLLKLVEIQESSHIEVPI  
 FKQFHKFVIGKGGANIKKIRDETQTKIDLPAEGDTNEVIVITGKKENVLEAKERIQK  
 IQNELSDIVTEEVQIPPKYNSIIGTGKLISSIMEECGGVSIKFPNSDSKSDKVTIRG  
 PKDDVEKAKVQLELANERQLASFTA EVRAKQQHHKFLIGKNGASIRKIRDATGA  
 RIIFPSNEDTDKEVITIIGKEESVKKAREQLEAIKECDEVTEGEVSVDPKHHKHFA  
 15 KRGFILHRISSECGGVMISFPRVGINSDKVTIKGAKDCIEAARQRIEIVADLEAQT  
 IEVVIPQRHHRTIMGARGFKVQQVTFEFDVQIKFPDRDATEPVEGLTNGGSGENG  
 GENEGQEGEQEVEKEAEQEPVRQCDVIRITGRIEKCEAAKQALLDPIEEELSVPF  
 DLHRTIIGPRGANVRQFMSKHDVHVELPPSELKSDVIKVCGTPARVAEAREALVK  
 MIEDYEADRADRELRSFVLQVDVDETFHSLIGRHGAVINKLRADHDVIISLPKRD  
 20 EPNDRIISITGYQANAEAARDAILEIVGDPETLHREVIEIDKRIHPHLIGQRRRTIRKII  
 EDNKVNIKFSADDDNPNSIFISGKIEDVENVKELLFGMAEDYERDYLDNVAIAPPTI  
 GAFLTGFWIRCRRCQRRIRHQRRTVGEAKAGQKPDCAQHSVAGGLPALRCWRG  
 SGGLHAYHLRVGPQKLSASGRVSRSPA VAAILQVGVRRGSELEMDQELEQKLELE  
 LELDYRAMSGRAAAVVRTSL

25 >18:26:17|GENSCAN\_predicted\_CDS\_7|3963\_bp  
 atggaggaaactaacaacgaactaccatcgagcagcagcccatcgctctcattaatggccaagagcaggtggccaacgagca  
 gcaaccatcctcgccaacttcagtgccacgcccactagtagcggcggaactggcaatgccacaccgccttagctac  
 gacgacctgttccggccctgccggccaacttcggctcaatcgcaatccggagcttcgggttcgactctagctcgtgtgacgag  
 30 ttcccaaaaaactcatattgtgcatgttcctgcaaggagcgcaagtcacggagtcggagaagtttggcgaaggcgagtcgaag  
 cgtatttgcagcagatcaccaaggagaccggagccagatcgagattgccagtcggcaggtgaccgttcctcgggagcacttc  
 cgcgtcatcctcggcaagggtggccaacgggtgcgcgaaatcgagcgtgttactgcgacgcgcatcaacatcccagccagag  
 cgatgagagcgagtttatcacgattgccggaaccaaggagggtattgccaggccgagcaggagatccgtcagctgtcagccg  
 agcagtagacaagaagtcacgaccgcatcacgggtgccaaagtaccatcccttcacgtgggccctacagcgagaacctaaa  
 35 taagctgcaggaggagaccggcgtaggatcaacgtgccgccgagcaggttcagaaggacgagatcgtcatctcggcgag  
 aaggacgcggtcgacggcgaaggccaaggtggaggccatttacaaggatatgaaaagaagtgcctctaccgtcagtggtga  
 ggtagctaagcccaagcaccgatattgcttggcgaagggtccaccatcgccgagattctgcagttgaccgggtgtgtctgtag  
 agatgcctcccaatgactccccctcgagacgatacttgcgtggcgccgaagtggcttgggaaatgcctaaccgtgtctac  
 caaaagtccaactcgtcaagtctgtggagatcaatcgggcacattggatccacaagtatgtgttcggtcgcaagggggccaaca  
 40 tgaagcagctggaggaggactgccccacgtgaacgtgaattgcctggagacaagatcaagctggaggggagatcccagaa  
 cgttgacagggtcttagcctactgtccgaaatcatcaaaaactacgaggagaacttcacattcgaggtgatgacggttaatccttc  
 gtactacaagcacatcatcggttaaggctggagccaacgtaaatcgccctgaaggatgaactgaaggtaacattaacatcgaagag  
 cgcgaggggccagaacaacatccgtatcgagggtcccaaggaggagtagcgccagggcgagcttgattacaagaaaaatcg  
 aaaaactggaaaacgaaaaatgaaggatgtgatcatcgaccgccgtctcatcgttctattatcgagagtaaggggcgagaagatt  
 45 cgcgaggtgaaggaccgctaccgccaggttacaatcacgatacctacgcccagagagaataccgatattgtgaagctgcgcgg  
 acccaaggaggatgtggacaagtgtcacaaggatctgcttaagctggtcaaggagattcaggaatcgtgcacattatcgaggtg  
 cccatcttaagcagttccacaagttcgttattggcaaggcgccgctaacaatcaaaaagatccgcgatgagaccagactaaaat  
 tgatctgcctgccgagggtgacaccaacgaagtatcgtaatcaccggcaagaaggagaacgtgctcgaggcggaaggaaacgta

tccaaaagattcaaaacgagctttccgacattgtcaccgaggaggtgcaaatcccgcccaagtactacaactcaatcatcggcact  
 ggccggcaaaactcatctctc gatcatggaggaatgcgggtggtgtttctatcaagttccccaacagcgactccaagagcgataaggt  
 cactattcgcgggtcccaaggacgatgtggagaaggctaagggttcagctattggagctggccaacgaacggcgagctggcttcctt  
 accgcccaggtgcgcgccaagcagcaacaccacaagttcctgatcggcaagaatggcgcttctatccgtaagattcgcgatgcc  
 5 actggtgcccgcattatcttcccttcaaacgaggacactgacaaggaagtgatcaccatcattggcaaggagaagagcgtaaaga  
 aggcccgtagcagctggaggcgatcatcaaggagtgcgacgaagtaaccgaaggtgaggtttctgtcgatcccaagcaccac  
 aagcacttcgtggccaagcgtggcttcacctgcaccgcatttcggaggagtgcgggcggtgtagatctccttcccccggtgcgg  
 catcaactccgataaggtgacgatcaagggtgccaaggactgcattgaagcgggcccgccagcgcatcgaggagatcgctgccg  
 atctggaagcgcagaccaccatcgaggtggtgattccacagcgctcatcgcaccatcatgggcgcacgtggatttaagggtca  
 10 acaagtcacctttgagttcgatgtgcagatcaagttccctgatcgtgatgccaccgaaccgctcgagggtctgaccaacggaggc  
 agcgggagagaatggaggcgagaatgaaggccaggaggagagcaggaagtagagaaggaagccgaacaggagccgggttc  
 gtcagtgcgatgttatccgaatcacgggcagaattgagaagtgcgaggccgccaacaggctctgcttgatcttccccatcgag  
 gaggagttgtcgggtgcctttcgacctccatcgtaccatcatcgaccgcgcgggtgccaatgtgcgtcagttatgtccaagcacgat  
 gtgcacgtagagctgccacctagtgcgttaagtcggatgtgatcaaggctcgtgcgggtacgcccgtcgcgtcgccgaggccgcg  
 15 gaagcgtggtgaaatgattgaggattacgaggctgatagggccgatcgtgagctgcgctccttcttctccagggtggacgtaga  
 tacggaattccattcgaagctcattggtcgtcatggcgctgtgattaacaagctgcgtgccgatcacgacgtcatcatttcgtgcct  
 aagcgggatgaaccaatgaccgcacatctctatcaccggctaccaggccaatgcggaggcagccgcgatgccatcctaga  
 gattgttggcgaccccagacacttcacgcgaggttatcgagatcgataaacgcaccccccacctcattggccaacgcgga  
 cgcaccattcgcgaagatcatcgaggataataaggtgaacatcaagttctcagctgatgatgacaaccccaattcgatcttcacgt  
 20 ggcaagatagaggacgttgagaacgtcaaggagttgctcttcggcatggctgaggactacgagcgtgactacttgataacgtg  
 gcgatagcggcccaacgattggtgccttctaactgggttcttgatccgatccgcagggtgccagcgagaacggattcgtcatc  
 aaagacgcaccgtgggagaagcaaaagcaggccaaaaaacctgactgcgccaacactcagtcgcaggaggacttccgcact  
 tcgctgctggcgggggtccgggtggcctccacgcctatcacctccgtgtgggggccccaaaaactaagtcacatcgggccgagtgte  
 ccgatcggcagcagtagcagcaataactacaagtcggggtgcgccggggatcgaggctggagatggaccaggagctggagca  
 25 gaagctggaactggaacttgattgattatcgggcaatgagcggcagagcagcggcagtcgtgcggacatctctttag

***Drosophila* Gene Hit** BLASTN with rescue sequence 1: dodeca-satellite protein 1 (DDP-  
 1) (AJ238847). TBLASTN with ORF2:dodeca-satellite protein 1  
 (DDP-1) (AJ238847).

30 ***Drosophila* EST** GH20785 (AI389573), LP07358 (AI294065)

**Annotated *Drosophila* genome genomic segment** AE003799

35 **Annotated *Drosophila* genome Complete gene candidate** CG5170 - Dpi dodecasatellite  
 DNA binding protein  
 CG5576 - Bg5 involved in  
 cytoskeleton organization and  
 biogenesis which is putatively  
 a component of the plasma  
 40 membrane

**Human homologue of Complete gene candidate** CG5170- 4885409  
 ref|NP\_005327.1|pHDLBP|  
 high density lipoprotein  
 binding protein  
 45 >gi|2498434|sp|Q00341|HB

5

CG5576- 2e-07 4506539  
ref[NP\_003795.1|pRIP|  
UNKNOWN >gi|3426027  
(U50062) RIP protein kinase  
[Homo sapiens]

10

**Putative function** CG5170: DNA binding protein (homology with Scp160p, a new  
yeast protein associated with the nuclear membrane and the  
endoplasmic reticulum, is necessary for maintenance of exact  
ploidy)  
CG5576: death domain containing protein, possibly involved in  
signal transduction

15

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**Confirmation by RNAi** CG5170: Reduced G1 and G2/M peaks indicating fewer  
cycling cells and more polyploidy  
CG5576: Loss of G1 peak

**Example 63 (Category 5)**

**Line ID** 40/2  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** NR  
**Map Position** 39B

**Rescue ID** BamH1

**Rescue Sequence 1**

TTTTGCCTCCGCTTTTAAATTAATAAAAAATGTNTGTTTNGCCCTGGAGCTCTCG  
 10 GTCTGTTAGCGAGCGTTGCCACCTTTCTGCGAGCTGTTGCTGCACACTGCCACT  
 TTACGAACACAGCTCTGATAGCGGGACAAAATACGTCAAGGCAGCGACGGTG  
 GGTTACTAGTGAATTTGGAACGGTGGTCTTAAGACGTACTGGTCTTTTATATTT  
 TCATTATTTTTTAAATTGTCGCTCATTTACCAATAAACCTTTTTACTTTTTCTCG  
 ATAGTCCGAAGTCAGATCAAATAGGAAGTTTCACAAAAAATTTTCATCCAGAG  
 15 AAAATACGCCGACGCTATTCGAGTTTTTTGTATTTCGTTAACCAGGAAAGAATA  
 GTTCGAATTCGTTTCGCACTTTATCGATAGTAGATTGCTATTATGGAGCCCACTA  
 GTAAATTAATTAATTCAGACTGATAAAAGCGATCAACTTTTGTTAATGGGT  
 TTAANTCTATAATAATNCTTAGTCCAAATTGTNTCAAAGTAGTCGATAATTTAT  
 AATAACAGTTTTAGATGACCTCTAGGAAATAACTAATTACCCACATNCTTCAA  
 20 GAAAGTGTTNCAATTTGTNCTATAATTAAATAACAGTTGTATTAATTATGTTG  
 TNATTGTNACTCATAATACAAATTAAACAATATAAACACACATAAATAAGAG  
 AATTGGAATATTTTGTCTCAGATTAGATTTNCCAC

**Rescue ID** EcoR1

**Rescue Sequence 2**

AACGGGGGGCTTCCGCGNCNCCAAAACGCAATNTACCGTTCATGCTGTGAAG  
 CGAAAAAGAGTGGTAGCGCCTACCNTGGCATATGTAGTTAAATCCGTGAAAT  
 AAGTGAATAAGAATATATGTATGTACTTAATTCGAAAACCTTTTCGCCGTCAG  
 CACAACGGGTGAACGAGAGAGCGGAAGTGGAGTTTTTTGTGGCGGGTTCGTCT  
 30 CGCTCGCACCAGCAAANGTCGTCCGTGGCTGCGTGTATGGGTGTGTGGAAAAA  
 GCGTCGAGGTGAATGTGGATTTCTAACCACACCAGCATTGCAAAGACATTGAT  
 TGATATTTAAAGCTGCAGCAGCGAACAAAGCAAATCCTAATTTCCGGCAAAGTT  
 TAAGAATAACGAGTGACTGGGGCGCGCAATAAGATAAAATTGAAGGTTAT  
 CTGTGTGCGTGTGAGTGACCGTNTACCAGTGTGTGTGTGCGANCGTCCATTGT  
 35 AAACAAAAACAAGTGTGTGAGCGGAGAGAAAGAAAGGGAAAGAGAGAAAG  
 AGCGAACAGACTGGCGAGAGAAAAAAGAGATGCCACAAANAAAGCAGCGCA  
 CAAAGGAAAGCTGAAAATTTTCAATAATCTGCAAAAGTGAAGAAAACCACAA  
 GAACCCGCAGTCNTGTAAATAAAACCCAGANTCCAAGAAACNTTAAAGAA  
 GCAGTGCAACAACTGGTGCTNTGAATGCGGTTTATTTTGAAAAAAATGCA  
 40 ATTCGGTCCGATGGAA

**Genomic hit, Accession No.** CSC:AC014744

**Drosophila EST** several including LD46342 (AI544109 BLASTN similar to mRNA  
 45 L07550)

**Annotated *Drosophila* genome genomic segment** AE003669  
**Annotated *Drosophila* genome Complete gene candidate** CG8678 - novel with ankyrin  
homology

5 **Human homologue of Complete gene candidate** CG8678 -gi7661580  
B69CEC399B56F35C  
|ref|NP\_056425.1|DKFZP434J  
10 154 protein [Homo sapiens]  
(2.20E-85)

**Putative function** Novel protein with ankyrin domains, unknown function

15 **Confirmation by RNAi** Reduced G1 and G2/M indicating fewer cycling cells

**Example 64 (Category 5)**

**Line ID** 55/12  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** NR  
**Map Position** 49C

**Rescue ID** BamH1

**Rescue Sequence**

10 TCTCATGNTCAGGGGGCCTTTACNATGTCAAAGAGCAAATTGTCCACAGGGCA  
 GCAACCGCAAGTGAGAGACGGGTGGAAAAC TGGGCGGCATGACCATGAATGA  
 AAGCCGCGACCGGCAAACGTGGCCCGCCACAAAGCGAGCATTTTCACATTTT  
 AACTGTCTGGACATTTTGTAAAGTTACACCAAGGCAATGATACCAGTAAAAAAG  
 AAGAAACAATCATTTTGAATAGATTAATCACCTGATTAATGTTGGTTGTATGT  
 15 TGATTGTAGGTGTTTTAATATACAATGTCTCTATTACTGCTTTCCTTTATTCAA  
 AGCCATGTGTAAGTGTAAGTTCTCGATTTCGGCTAGATTTTGAAGTTCTGCCAT  
 TATCAATTAAGTCCAGTTCCTCTATAAATTGGTAATAAAATAGCTCTTTACA  
 GCCAAGTATATGTGCAATTTTGTAAAGATTAAANGTCCAAATGTTGTGAACCTT  
 TCCTGGCCCTGAATTTTAAAAAACCATTAATTTGGTCCCATTGACATTAAATG  
 20 TTCTATGTACATTAATATGACTTTTTGTGGATGGTTTTATAACAAGCATTACT  
 ATATTCTAAAAATCAAGGATAAAGGACNAGCTTTACAGGAGGTAACATTCCTA  
 TTGTACGGCTTTATTTTCTTATACCCATAAGAGCATACCACTAGGATCCGTCGA  
 CCTGCAGATCTCTAAAAACTTGCCTTTGCTGGCGTTTTCCATAA

25 **Genomic hit, Accession No.** AC007085

**Associated ORF**

Genscan ORF1 predicted sequences >21:54:11|GENSCAN\_predicted\_peptide\_3|108\_aa  
 MGLVTAAFKLKRKDIQDRYQHDINRICHTRSTAHTAYAHFAEHLLRRSPRQRFVN

30 GKGAALVLILLVSAARQFSGSTGAYKLGNRVKGVEGEQQEYKLQDRTTTHFCGN

>21:54:11|GENSCAN\_predicted\_CDS\_3|327\_bp

atggggctggttaaccgcccgttcaagctgaagcgcaaggatatccaggacagatatcagcatgatattaaccgcatctgccaca  
 cacgtagcacggcacacacggcgatgctcattttgcgagcatctgttgcgacgaagtcacgtcaacggttgtcaacggcaa  
 35 aggtgctgcgcttgctcatcctcctcgtttctgcggtcgcacaattttctggctcgacaggtgcctacaaactgggtaataagagttg  
 gaaaagtagaaggggaacagcaggaatacaaaactacaagacagaacaacacattttgtggcaattaa

Corresponds to CG8732

40 **Annotated *Drosophila* genome genomic segment** AE003836  
**Annotated *Drosophila* genome Complete gene candidate** CG8732 - l(2)44Dea  
 homology to fatty-acid-  
 Coenzyme A ligase, long-  
 chain previously described  
 45 spindle/chromosome

abnormalities in neuroblast  
squashes

**Human homologue of Complete gene candidate**

5

1e-171 4758330  
ref[NP\_004448.1|pFACL3|  
fatty-acid-Coenzyme A ligase,  
long-chain 3  
>gi|4165018|dbj|BAA371 and  
LCFD\_HUMAN LONG-  
CHAIN-FATTY-ACID--COA  
LIGASE 4 1e-157

10

**Putative function**      Fatty acid CoA ligase

15

**Confirmation by RNAi**      Only wild type profiles observed

**Example 65 (Category 5)**

**Line ID** 6/7  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** NR  
**Map Position** 28E

**Rescue ID** BamH1  
**Rescue Sequence 1**  
10 TATNAATAATCATAGGGCTCTTGCTCTTACGTGTAAGGCCTGCCCTCTNCCA  
GTCTATATACAAAGAAAAACACACACACACTGGCACACTGGTGTTTCGCATATG  
CCAAAGCCGAGTTAATTTCACTTTGTTTAATCTATCGTTTGGTGTTTTTGCATTT  
TTTAACCGCGCAAACGGTATTTGCGCGTTTTGCGCCTCTTACTTTGCGATTTAT  
TGCACCGCTTGGCTGTGTTTTGCAATTTCTATCTTGATTTTCATTGGTATTCACG  
15 CGTAATGTAATTCTTAGCAGCGTGACCGCGCCGATAACGATAAAAAATACCAC  
GGGACCAAAAATAAATACCATATGATACCACTTCAGGGAAAAGAAATCCTAT  
TTAATACCACTCACTTTAAAAATAAGTTTTTAAAAATATATATNTTTATTTAAA  
AAAAGGTGTATTTATAATCAAATACTCGGTACTTNTTAATTACTCCAAGAANA  
ATTAATTTGAAAAAAAGGGGTTCATTATAAAATATATATTAACCGCTTACAC  
20 ATAATCCCCAAACAAAACAGCGATTGGGATTTAAAAGGTTCTAAGTCCATCAT  
TATAAAAGATCATTTCCGAAAAACAAAAGAAATAGATTCAAAATTAGGCGAC  
ATCAGCCCGCTGATAANGATCATAAAAAATACAGAAGCTNATTCAGCGAATCA  
GAAANTCCTACTCGCCACTATCCGAAAAACNTNGAAAAAAAATGG

25 **Rescue ID** EcoR1  
**Rescue Sequence 2**  
TGAAAGGTAGCAACAACGTTTCCTTGAAAAAGCTGTAAATAGTAAACAAAA  
TTGTCAAGTTAACGAGCCAAAGTTATTAAATAAGGTTTCGAGTACGTTGGCATC  
GGCTGCCCAGGCAGCAAANAAAAACAAAGACGCAGTTCAAGATCAGCTGGAC  
30 ACTTAGAAGANTTTAAGAATTGAAGCACATTNNAAGAAAGANAAACAAGAAC  
CCCACCAAAAACCCGCGTGCGTTTTGTATGTGTGTGTGCCATCAAATTTCCCGC  
ACTGGGTGAATGTGCNTGCGTGTGTTNTGTGTGCATTTAATTTTCTACCAATAA  
TCGCCTTCCAAGAAGTGAATACCAGCCGATCCACCGCTAAATCGAAAAAAGTT  
TNACTCTGGGTTAANTCACTGTTTACGGCTTTTGTGCTATAATTACCTTTCCCG  
35 TAAGCNGTGGAANCTAAANCCAAAACNTNAGAATCCGAATTCCG

**Genomic hit, Accession No.** CSC:AC017934

**Associated ORF**  
40 Genscan partial ORF1 predicted sequences  
>22:35:21|GENSCAN\_predicted\_peptide\_4|128\_aa  
MGTNSGATAGINNKPVGATGAGVLVGGGVGGANSSIGGVLSNSLGGGGSGGLS  
ISGLNAGGQNaNVGGMGNVGGDDGGNGMVGGGVNNQQATTPQYTIPGILHFIQ  
HEWSRFELERSQWDVDRAELQ  
45 >22:35:21|GENSCAN\_predicted\_CDS\_4|384\_bp

190

atgggcaccaattcgggagccaccgctggcataaacaacaagccggttgccggtgcaacaggagccggcgctcctttagggcg  
 gcggtgtggcggtgccaattcctcgatcgccggtgtcctgtcgaacagcctggcggtggcggcagcgggcggtctgagcatc  
 agcggcctcaacgctggtggacagaacgccaatgtggcggaatgggcaacgttgccggcgacgacggcggaacgggatg  
 gtggcgcggtgtaaataaccagcaggccacaacgccccatacacaataccggcatcttgcaattcatccagcacgagtgg  
 tcgcgcttcgagctggagcgatcacagtgggacgtggacagggccgaattgcag

**Human Homologue** TBLASTN with ORF1: very weak homology with striatin,  
 calmodulin-binding protein (STRN) (NM\_003162.1)

**Drosophila EST** several including LD42534 (AI516610), LD03224

**Annotated Drosophila genome genomic segment** AE003619

**Annotated Drosophila genome Complete gene candidate** CG7392 – novel WD40 family  
 member

**Human homologue of Complete gene candidate** CG7392- SG2N\_HUMAN  
 CELL-CYCLE NUCLEAR  
 AUTOANTIGEN SG2NA  
 (S/G2 ... 622 e-178 A cell-  
 cycle nuclear autoantigen  
 containing WD-40 motifs  
 expressed mainly in S  
 and G2 phase cells

**Putative function** WD40 protein a novel nuclear protein mainly expressed in S and  
 G2 phase cells that was characterized using autoantibodies from a  
 cancer patient

**Confirmation by RNAi** Reduction of G1peak , more polyploidy

**Line ID** 103/1

**Category** 2nd chromosome, small imaginal discs

**Reversion** R

**Map Position** 57B

**Rescue ID** BamH1

**Rescue Sequence 1**

GATTTCAA AATTAGGCGACATCAGCCCGCTGATAAAGAATCATAAAAAATACT  
 GAGGCTTATTTTAGCGAGTCAGAGACTCCTACTCGCCAACTATCGAAAACATA  
 GNGAAGATATAGTCGCCAACCGATCTGCCTTCTATAGTGTTGCTTATTGTTGTC  
 CCCTAATCAAATTAATAAAAAATCTGCATTAGGCTGCTTCGCCGCCAGCAACA  
 AATGTTTTACACCTACTGTACTTTTCGCAGAACAGAGATCCAAATGCAGGATC  
 GTTTCATGACTGTACATTTATTCGGATTAGACATTAAATTACACCCTACAGCT  
 ATACATACTAACAGTGAACACGGCAAATGCTTAGCTAGCATTGGGCCACTTTC  
 GTTGACTGCGAATAAAAAATGATTGGCCGATGCCTTTAGCAGATTCTTTTGAT  
 CGAATTACTCGGATGGCTTGTGTGTCCACCTCTTACAAGAACTCCTCGCACCA

ATCGTTGAGACAGTTGTAGCAATCGGATGCTTGGTTGGAGCTGGCGTGGCACA  
CCTTCTTCATCCAGTCCTTGGACAGNTTCTTGGNCCTTTTCAGNANCAGGATCT  
GGTCCCAAACGGNGGAAGGCCTAAAACGAATGGNAATTGATCGGTAGCCCTT  
GACTGGCATTGGTAATTTGCGCACATGGGNGTCATCGGATTTACACACGCACC  
5 ATATCGAATCAGCGTCCTTAAGCGTCAACCGAGGGTTTCCCAATTCCGGCCA  
GTTCCGTCACCGACTTGGTTGCCATTGG

**Rescue ID** EcoR1**Rescue Sequence 2**

10 ATCAAAGCGNCTGGGCCCCGTGCATCGCCNCAGCGTTCGTCTTAATTAATTAGT  
GATTGCAAGCGGGTGCAATTATGCACAAAATTACGGACTAATACAACCTGCCC  
GCTTCGCGCTCTCTCCATCTCCCTTCCAAATAGTCGTTTGCTCTTCGCACACAA  
AAGTGTA AACCTGTGAAAGGTAGCAACAACGTTTCCTTGGAAAAAGCTGTA  
AATAGTAAACAAAATTGTCAAGTTAACGAGCCAAAGTTATTAAATAAGGTTTCG  
15 AGTACGTTGGCATCGGCTGCCCAGGCAGCAAAGAAAAACAAAGACGCAGTTC  
AAGATTCAGCTGGACACTTAGAAGAGTTTAAGAATTGAAGCACATAAAAAAG  
AAGAGAAACAAGAACCCACCAAAAACCCCGCCGTGCGTTTGTATGTGTGTG  
TGCCATTCAAATTTCCCTGCACTGGGTGAGTGTGCGTGCGTGTGTGTGTGTGTC  
AGTTTAATTTTCTACCAATAATCGCCTTTCCAAGACGTGATTACCAGCCGATC  
20 CACCGCTTAAAATTGATAAACGTTTTTAACCTTTGCGTTACATCAGCTGTTTTAC  
GGCTTTTTTGTGCTATAAGTTACGTTTTTCCCGTAAGCCGTTGGCAACACTAGAA  
CGCAAAAGAGCATAAAGAATCGCGAGTACCGTANAGAGGAAGAGAGGAAGA  
GAGAGAGATAGAGAGTGTGAGCGTGTGAGTGAGCGGGGAATGTGGGGGCGGT  
TCCGGTGCGAAAAAACGTAGTAGTAGTACATNNAGAGAGTGCGAACGAGAGG  
25 GAGGCAGCCAGCGAGTGTCTGCGACTGCTCCCCCCTTTACCCTCGTCGCTTTT  
CTATTCGGAAAATTCAATGACCTCATTTGTTTCATGTGCGCGAACTTTGCTTTTC  
TTTCCCAACCTAAAAACGCAAAAAAAAAAAAAACNCCAAACAGGATATACGTNG  
GAACANTGANCAACNANTTCGANAAAACCAACAACNANGGACCGTGCCCTG  
GGGCNCCTGAAAGGCAAACAGCTGGCNCNCAAATCCGGAAAAGGATCNGGAA  
30 NAACAGGATCNGCGGGCNCAAGGATCNC CGGAACAGGCAAAGGAAACNCCC  
GGCNCACNGCACAAGCCNCTGAAAAGCAACNTGAACCAATGGGCACCANTTC  
CGGGANCCACCGCTGGCATTA

**Genomic hit, Accession No.** CSC:AC017934

35

rest of results as for line 6/7

**Example 66 (Category 5)**

**Line ID** 65/24  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** NR  
**Map Position** 48A

**Rescue ID** BamH1

**Rescue Sequence**

10 TACGATTTTGCANTGCNCCATTTTCGTGGCACCCGATTTGTATATATATTTTTT  
ATATAACCCACGGATTGCCAACTTTCATTGCCCTTTCACACTCTTATTCGCCAT  
TTATGAACTCTTCTTTGACGATTGGAACGGTTCTTTTTTCGCTATTTTCGACTGC  
ACCCGCGCTCTTTTCGCTTCGCTCTCCTCCCTCTCTACACACCGCTCTTTATCCT  
TAATTGCTTTTTTCTATTTAGCGGAATTGATCGTTCTCAACTTGGTCGCCATTGC  
15 AGCTCCACAGGCGAAAAAATCGGTGGAATGCCAATACAGGTGCACGGCGAG  
TGCCGATAAGCTGGAATAATCGGGAAAACGCACGCCTACACATTCATTGCCAG  
CATCGGCTTTGCCCTTTTCGCTGTCGAGATTAGCATATTTCCACTTTTGGTTCGC  
GCACAACACTANCTAAATTATTGNTTATTTTTTTCCCAACTGTGAGGTGAAAC  
TGTGAAACAAAACCACTGTGGGCGGGTCAGTGTGACCCTCTCGCGGTGGGTG  
20 AAAATCCTAGTGAGCTTCGTTGTTAGGGCTGTATGACACGAAAGCAAGTTGAA  
AAGAACTTTTTTAAATTATATTGGTTAATTGAGCAGAACTAAACTATATN  
AAAATATTTAAGAATNCAGATTAGTGATGTATTTAATAATAATAGTAAGAT  
GTTC

25 **Rescue ID** EcoR1

**Rescue Sequence 2**

CTTNTTTGATAGANATAGGCTTCTTTTAAAAAANAAGCAGCANCAGGGG  
CCNGAAGTGCGTGNNTGTGAACGCTGATTGCTTGCAAGTGTGTTTCGTGTGTG  
TGTGATTGTGTGCTCCGANCAAGTGAAATCAATAATTTGCAGCCACAAGCA  
30 ATTAATAAAAACTGCAATAATGTCAAAAAATCTAATTGAGGCAACAAATTAN  
CAAAGCCATNAAAGCAGGCTGCACTGCGAGAAAATTGTGCCTTTCCACAGAT  
CTTCTGCTGCAAAGCNAAAGAANGTAAGCAAGTCGGCCANTTTATTNCATTCT  
TCTCATCTCTCTTCTTCGCGAATTGGCGCNTANCACTTACAATAATTNATATNA  
CTTCTTAAATTTCAAANTCCCTTTCNTGAACGGANCTTTTAACGGAAAACAAA  
35 GCGGGTAACTAACTTAACTAACTAATTANAANTGTANGTATAAATGAACC  
GAACTCGCTTTAGATATNATGCGTTTCACTAACANATTANAACAACTTTGAA  
GCTGTANTGTCAGGTTGTTATTNCGTTCACCANATGTAGACTGNCCGNNAATT  
TNACCTTTCCCATANTCTGTTCTTAANTGTNTTGTTTTTTCCCAATNNTTGTATC  
ATNCNTTGGTNAATNANCTNAACGGCCCAAAGTNAATGAATTCANTCACGTG  
40 CACTGGCTCTGGTTCNATANTTAATNGGCTGTTTCTTACTTCCCTTAACCCTAA  
CATCTNTTAATCACCTGTGCCATNTGTTTGTGTGTGTGTGAACGAATGAGAAA  
AAAAA

**Annotated *Drosophila* genome genomic segment**

AE003825

**Annotated *Drosophila* genome Complete gene candidate** CG9005 - novel putative cell adhesion

**Human homologue of Complete gene candidate** CG9005- Ensembl predicted gene  
ENSP00000006008  
Gene:ENSG00000005238  
Clone:AC004472  
Contig:AC004472.00001 6.00E-38  
(KIAA1539 protein AB040972) and  
AK022837 Homo sapiens cDNA  
FLJ12775 4e-33

**Putative function** Putative cell adhesion protein

**Confirmation by RNAi** Reduced G2/M peak

**Example 67 (Category 5)**

<b>Line ID</b>	74/3
<b>Category</b>	2nd chromosome, small imaginal discs
5 <b>Reversion</b>	NR
<b>Map Position</b>	47A
<b>Rescue ID</b>	EcoR1
<b>Rescue Sequence</b>	
10	GCACAGAATGGCNCCTTCACGACAAAAGATCTNCNAATTAGGATGATGCAGA AGGAGGACACGCTTTTCATTATCTGGTTGCCACCTAATTTAAGTTCCACATCAA GGGAAGAAGGAAATACGTTCCAACGGACGTCAAATTTACTAACTACACTACTT GAAAAGCCTGTCTATAAAAAACACGATAACGTTTTTGTCTAATCTCAAGACAATG TTAAATATAATTGGAGAAAGTATTGAATATGAATATCACAAAAATTGTTTAGG
15	GTCTCTACGTGGTAAATAGTATTTGGCATAGACAGTGAGATGTGAGTCGTACG TACTAATTAATAAAGTTGTTCAARAGAACCTCATATACTGTAAGTGACAACGA ACGAAGCTGACAACCTCTGCTTGCACATATTTGGCGGAGTTCGAAAATATCATC GCATTGGTATTGTTTTTGTNTCCACCNTGGGGCGAGATTTTGTGTTGCTTTAC TTTGCTTGTTTTTTCNCCACAAANCGAACCATAATGTTTCGAAATGGTAAAATTA
20	CCGTGCCAACAAGCTCTCTCTCTCCCACTCCGAACTCTCTCATCTCTCCTTG CAATTGTTTAAGGTGTGCAAGGAAATGAAAAATGTCCCGGCTGTGTTNCCATG CATTCCCCTTCAAAGCCAATTATNTTTGTGCCTCTCCAACNTTTTGTATCGGNN TGATTTTTTTGGCTCCCCNTANTCCCCCCCCCTTCNCCCATTCCGGGTTANAT TATTNTNCCAATTTTCTATTTTACGGTCCCNNGTTCCCTGGAAATANTTCCTNC
25	AATCNCCGCTCCATNTCNCCATNTTTGACAGATTTTC
<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003829
<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG12052 lola -a specific RNA polymerase II transcription factor involved in axon guidance
30	
<b>Human homologue of Complete gene candidate</b>	1e-09 3789797 (AF059569) actin binding protein MAYVEN [Homo sapiens]
35	
<b>Putative function</b>	lola-like specific RNA polymerase II transcription factor
<b>Confirmation by RNAi</b>	Almost no G1 peak and increase in G2/M peak indicating arrest in G2/M
40	

**Example 68 (Category 5)**

**Line ID** 79/7  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** R  
**Map Position** 55B

**Rescue ID** BamH1  
**Rescue Sequence 1**

10 GTCTCATGCACCCTGGCCCTNAGCTGCATAAGTGTAAGTGTGTGNCTGTGTGC  
GAGTGTGGGTAGGCGGCGGCAACTATCTCGCTTGCTCTTGCGTCCGGGGTTAT  
CGGTAGCTTCTTCTAGGCTGAGTGCATTTTCGTTGAATCGTGGATGTTGAAAGTT  
GTCTAATTTCCGAACCTATTGATTTTTTCCCCTTCCCCGTCAAGAACTGCATTGT  
TGCTTCTTGAAGACCAGTTTTTGGTAACATCAGGAGAATGGAAAGGAGCGAGT  
15 GAGTCGGTGAGTAAGTGAGTGAGCGATGCGAGCGACAAAATCAACAACAACA  
ACAACAACGGTCAAAACGAGTTCCAACGAAAGTTGCAACACTCTCAACAATT  
TGAGCAGCTCCGTTTGTGTATTGCACTTCAATCGGGAAGACTCTACACTC  
GACGGAATAGTGTGCTCGTCTGAAATTTATCNATTTCCATTCCCTTCCTTTGTTT  
TTGGGCCAAACAATGGCNTCGGCAANCGTTCGTGGAAAACCGCAGGAACCAC  
20 CAAAATGCCTGGCGTCACATTAACCGAGCCGCCTTTGTTTATGCAAATATTATT  
GTAATATTTGGTNAAAATTAAGTCGCGCTTCNCGTTACTTTTTATTTCATATAC  
ACGCAGCAGCAGCACGCATACAGTCACGTCACGCACACATACAATCGCCGTN  
CACATACACTTGTCTTTTTNCCACACACTTTCCTAATCAT

25 **Rescue ID** EcoR1  
**Rescue Sequence 2**

NGNGTCTCATGCACCCTGGCCCTNAGCTGCATAAGTGTAAGTGTGTGNCTGT  
GTGCGAGTGTGGGTAGGCGGCGGCAACTATCTCGCTTGCTCTTGCGTCCGGGG  
TTATCGGTAGCTTCTTCTAGGCTGAGTGCATTTTCGTTGAATCGTGGATGTTGAA  
30 AGTTGTCTAATTTCCGAACCTATTGATTTTTTCCCCTTCCCCGTCAAGAACTGCA  
TTGTTGCTTCTTGAAGACCAGTTTTTGGTAACATCAGGAGAATGGAAAGGAGCG  
AGTGAGTCGGTGAGTAAGTGAGTGAGCGATGCGAGCGACAAAATCAACAACA  
ACAACAACAACGGTTCAAAACGAGTTCCAACGAAAGTTGCAACACTCTCAAC  
AATTTGAGCAGCTCCGTTTGTGTATTGCACTTCAATCGGGAAGAACTCTA  
35 CACTCGACGGAATAGTGTGCTCGTCTGAAATTTATCNATTTCCATTCCCTTCCTT  
TGTTTTTGGGCCAAACAATGGCNTCGGCAANCGTTCGTGGAAAACCGCAGGA  
ACCACCAAATGCCTGGCGTCACATTAACCGAGCCGCCTTTGTTTATGCAAAT  
ATTATTGTAATATTTGGTNAAAATTAAGTCGCGCTTCNCGTTACTTTTTATTTC  
ATATACACGCAGCAGCACGCATACAGTCACGTCACGCACACATACAATCGCC  
40 GTNCACATACACTTGTCTTTTTNCCACACACTTTCCTAATCATNNTA

**Genomic hit, Accession No.** AC004296

**Associated ORF**

45 Genscan: ORF2 predicted sequences >15:31:31|GENSCAN\_predicted\_peptide\_3|109\_aa  
MVTsFRHLRDEKSFTDVTLACEGQTCKAHKMLVLSACSPYFKALLEENPSKHPIIIL

196

KDVSYIHLQAILEFM YAGEVNV SQEQLPAFLKTADRLKVKGLAETPSSIKREG

&gt;15:31:31|GENSCAN\_predicted\_CDS\_3|330\_bp

atggtgacctcggtccggtcacctgcgcgacgagaagagcttcacagatgtaacactcgctgcgagggccaaacctgcaaagcc  
 5 cacaaaatggtgctttccgcttcagtcctactttaagcgctactggaggagaacccatcgaagcatccgatcattatcctgaaa  
 gatgtctcctacattcacctacaggctatactggagttcatgtacgcgggtgaggtgaacgtgtccaggaacaattgccagcattt  
 cttagaccgccgatcgctcaaagtgaaggcctcgagagacaccagttcgataaagcggaagggtga

**Drosophila Gene Hit** TBLASTN with ORF2: several zinc finger proteins including

Broad-Complex mRNA for BRcore-Z2 protein ( X54665)

**Human Homologue** TBLASTN with ORF2: kelch (*Drosophila*)-like 2 (Mayven actin binding protein) (KLHL2) (AF059569)**Annotated Drosophila genome genomic segment** AE003800

**Annotated Drosophila genome Complete gene candidate** CG5738- lola, lola-like  
 putative kelch-like putative  
 specific RNA polymerase II  
 transcription factor known to  
 affect disc morphology

or could be CG10914 - novel  
 unknown

**Human homologue of Complete gene candidate**

CG5738- 9e-09 3789797  
 (AF059569) actin binding  
 protein MAYVEN [Homo  
 sapiens]

CG10914- predicted gene  
 ENSP00000051207

Gene:ENSG00000047313

Clone:AC068261

Contig:AC068261.00019

4.00E-49 (potential cell  
 division GTP binding protein  
 1: ENST00000051207

**Putative function** CG5738: lola like specific RNA polymersae II transcription factor,  
 CG10914: Possible GTP binding protein

**Confirmation by RNAi** Both show marked reduction in G1 to G2/M ratio

**Example 69 (Category 5)**

**Line ID** 80/2, 81/8  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** R  
**Map Position** 57D/E

**Rescue ID** BamH1

**Rescue Sequence 1**

10 CANTTTTCAGAGGCCATAGNCCTTCACAAAATTCNCCATCTCTGCCCCGGCATCC  
 GTGCTTGAAAATGGTGCCAATGCGTCGTGGAGAATCTGCTGCACTCGATGGTC  
 TGCAAAAATTGCACATTTATTAGATTTAATAAAATTTTCAACTGTCCGCGANCAC  
 GTTTGCTCGTGTGAAATTTTCGAGTACAAAATTAGTGCGACTGTTGGATTGCATT  
 GAAATGCCAAAAATCGGTGTGACCATTTTGAAGTCCCCACAGGCTCATGACTT  
 15 TCGCGGTTACCAAATCCAAATAACGCAAGCTGGTCACGCTGTCAAACATCGG  
 TGACGGAATGGTGACGACACAAACAATTTGCTTAAAAACTTTCTTGCGGCCGT  
 AAAAATGCGCAAGCAGCCTGGCAGCGCAACGCACGTACACGTAATTGGAACA  
 AATGTTTGCTGAACCACAACCGCCCACTAAATGTTANCCGCCAAGTCTTTTCC  
 CCCGCCGCCGCCGTCTCNCNTCNCNCCGGATTATTTGGTTTACAATTTGCTTAC  
 20 ACAAGTGCAATCGTCGATAGCGCTTCATTTTGGAGTAACAAGTAATATTTTGC  
 GCCGTACTGCTGTTTCGCCGTATCAGACAGAAGGTTGGTATCAGTTCGACGCAG  
 CTTGTGACGGTATTGCATACGCGGCGAAACGCCACGTGAAAACGGATCGCA  
 GTTCTCGAAAACCTCNGGATAAAAA

25 **Rescue ID** EcoR1

**Rescue Sequence 2**

TGGGGTCTCANGCCCCGACGGCCATATTTTAACACAAGATTCNNCANCTCTGC  
 AGGGCATCCGTGCTTGAAAATGGTGCCAATGCGTCGTGGAGAATCTGCTGCAC  
 TCGATGGTCTGCAAAAATTGCACATTTATTAGATTTAATAAAATTTTCAACTGTC  
 30 CGCGAGCACGTTTGCTCGGTGTTGAATTTTCGAGTACAAAATTAGTGCGACTGT  
 TGGATTGCATTGAAATGCCAAAAATCGGTGTGACCATTTTGAAGTCCCCACAG  
 GCTCATGACTTTTCGCGGTTACCAAATCCAAATAACGCAAGCTGGTCACGCTG  
 TCAAACATCGGTGACGGAATGGTGACGACACAAACAATTTGCTTAAAAACTTT  
 CTTGCGGCCGTAAAAATGCGCAAGCAGCCTGGCAGCGCAACGCACGTACACG  
 35 TAATTGGAACAAATGTTTGCTGAACCACAACCGCCCACTAAATGTTAGCGCCA  
 ACTNCTTTTCCCCGCCGCCGCCGGTCGTCNTCNCNCCGGATTATTTTGTTTACA  
 ATTTGCTTACACAAGTGCAATCGTCGATAGCGCTTCATTTTGGAGTAACAAGT  
 AGTATTTTGCGCCGTACTGCTGTTTCGCCGTATCANACAGAAGGTTGGTATCAG  
 TTCGACGCAGCTTGTGACGGTATGCATACGCGGGGAAACGCCACGTGAAAAC  
 40 GGATCGCAGTNCTCGAAACTCNGGATAAAAGAAAAAGTAGGCTGAATG

**Genomic hit, Accession No.** AC007175

**Associated ORF**

45 Genscan: ORF2 predicted sequences >16:09:09|GENSCAN\_predicted\_peptide\_3|2497\_aa  
 MNEGNSAGGGHEGLSPAPPAVPDRVTPHSTEISVAPANSTSTTVRAAGSVGAALP

ATRHHQHIAATQVKGIASSSSKQKQLASAPVPLSPLPQQQQQTAEATAAAAAP  
 AHSNVSVSSSTIEASVLPPQAKRQRLDDNEDRTSAASIVGPAESSNIVSSLLPASVA  
 SSSEVGGLSSTALQDLNALKKRILQKQLQILRNLERHLENVSEYFYLQNGGSM  
 DYPAWRKKTPTPQFISYSNANRIDQLIHEDKPSTSAAAAAAQNQKYTTQQTDSVE  
 5 SSLVSGIGTGATKGAPLDGNISNSTVKTNTQSQVPSKIGSFTESTPAATESNSSTTV  
 GTATSGAATSTSATSASGNVLAVEAEIKIPAVGATPVAISTKLPAAVVQLTQQG  
 GTPLLPCNTSAGSTALRRPQGGQNNASSGSAAASGGGGSLTPTPLYTGNGPAALGG  
 SGGLTPGTPTSGSLLSPALGGSGTPNSAAQEFSEKAKQEVYVMQRISLQREGL  
 WTERRLPKLQEPSRPAKHWYLLLEEMVWLAADFAQERKWKKNAAKKCAKMY  
 10 QKYFQDKATAAQRAEKAQELQLKRVASFIAREVKSFWWSNVEKLVEYKHQTKIEE  
 KRKQALDQHLSFIVDQTEKFSQQLVEGMNKSVAADTPSLNSSRLTSPKRESDDDFR  
 PESGSEDDEETIAKAEEDAADVKEEVTALAKESEMDFDLNDLPPGYLENRDKL  
 MKEEQSSAIKTETPDSDDEFEAKEASDDDENTISKQEEAEQEIDHKKEIDELEA  
 DNDLSVEQLLAKYKSEQPPSPKRRKLAPRDPELDSDDDSTAVDSTEESDAATED  
 15 EEDLSTVKTDTDMEEQDEQEDGLKSLMADADATSGAAGSGSTAGASGNKDDML  
 NDAAALAESLQPKGNTLSSTNVVTPVPFLKHSREYQHIGLDWLVTMNERKLN  
 GILADEMGLGKTIQTIALLAHLACAKGNWGPPLIVVPSSVMLNWEMEFKKWCPG  
 FKILTYYGSKERKLKRVGWTKPNAFHVCITSYKLVVQDQSFRRKKWKYLILD  
 EAQNIKNFKSQRWQLLLNFSTERLLLTGTPLQNDLMELWSLMHFLMPYVFSSHR  
 20 EFKEWFSNPMTGMEIGNMEYNETLITRLHKVIRPFLRLKKEVEKQMPKKYEHV  
 ITCRLSNRQRYLYEDFMSRAKTRETLQTGNLLSVINVLMLQRKVCNHPNMFARP  
 TISPFQMDGITFHTPRLVCDIMEYDPFTQINLETNLNLLLHLEQTMAYVSHKSRL  
 APPRKLIEDIDTAPLPAPRCPNGKYRFHIRVRSALAQRILNAVKGASPAMRLE  
 GSKIMPMRNLPSGRVLKRVASINPVNMALKPVVINSVVTTSSTTASSPTGAL  
 25 SVLSNSKLLGARSQINAPTPAKVAKTMQDGKPFYLT PATNSGAAGARLTLSKT  
 TASASTTTSRTT VTASTTSGQQLIRDPIVKDLATHVKSTVQKQSIANGKTEPEEETE  
 AEDPYKVQELIQMRKEQRLAALKRMAMINRRRTDATPIYGEDCREAIQRCMQAT  
 RSLKRSTWQTRGYANCCTAMAHNRNGWSLNHLLKSFEERCADLKPVFANFVITYVP  
 SVCAPRIRRYVQNLSSTHWQHEQRIENVDQALRPKLALLHPIISEMTTKFPDPRLI  
 30 QYDCGKLQTMDRLLRQLKVNHRVLIFTQMTKMLDVLEAFLNYHGHYLRDLGS  
 TRVEQRQILMERFNGDKRIFCFILSTRSGGVGINLTGADTVIFYDSDWNPTMDAQA  
 QDRCHRIGQTRDVHIYRLVSERTIEVNILKKANQKRMLSDMAIEGGNFTTTYFKSS  
 TIKDLFTMEQSEQDESSQEKSENKDRIVATTTLSSTPSTVVETEKQSLRAFEHALA  
 AAEDEQDVQATKTAKAEVAADLAEFDENIPIATEDPNAEGGPQVELSKADLEMQ  
 35 NLVKQLSPIERYAMRFVEETGAAWTAEQLRAAEALEAQAQKREWEANRLAAMHK  
 EEELLKQETEAEMEMLTYSRKDSSNQVNTKTDSNSNKRRLVRENRRNSAQKLSRSV  
 SSHSTGSNNKNSKSATTRGNSQNSLNQTPVVGSGISRVNRTGAGVSSSSRGKSNST  
 KSTGKGTDAAAPQVRRQTRLHSLGAVNMAASARTPPTRKTTRTALAASAAASTLED  
 ASLIVEERPQRQSANIAMSKMMKTPFKQNVPSNISIKTTPPKRGRRDSVAAAATRS  
 40 KLLERRATIAAPLKHMDDESDQDEEEQEEQSEEDTEGEEANATVDDDEEGEEEL  
 ASLDEETIQTGSQTNDEEDDDDEEEVGEEGMVDIDTEDSEADVKSSTYGTADGK  
 PEEAESLDGWD AHDQVQDTTMTSSTYYNVSEESDTDEHHDSKAEAKEPPQNSDK  
 SDESEAVGHTPRTRSRGTVKINLWTLDVSPVANALNKSSANRSLKKAPRTESTPK  
 ESQSEPRRKITQPKLPKKEETNNKSNSNIGTLHRWISKSPRVMLRSTPVTAAASASS  
 45 AAVSGVSGGNASSSGTAR

>16:09:09|GENSCAN\_predicted\_CDS\_3|7494\_bp

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5 gaggacaggacgagtgcggccagcattgttgaccagccgagagcagcaacattgtaagctccctgctaccagcgctgggtggc  
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 5 agatgcgcaaggagcagcgattggcagcgcttaaacgtatggcaatgataaatcgctgccgaacggatgccactcccataacg  
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 20 cagaactgggttaacagctctcaccgatagagcgatagccatgcgctttgtggaagaaactggagcagcatggacggcgga  
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 ccatagcaccggtagcaacaacaagaacagtaaatcggcaacgacccgtggaaatagccagaacagcctcaatcagactgtac  
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 35 ggaatcagacacggatgagcatcacgatagcaaggcggaggctaaagagccgcccaaaattccgataagagcgacgagag  
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 gagccaaggcgaaagattactcagccaaagtgcggaagaaagaagaaactaacaacaaatctaacagcaatatcgccacctta  
 caccgctggatctgaagtcccccgagtaatgcttcgatccacacctgttacggcagcagcgctagctcatcagcagcagtgta  
 40 gtggtgtttcgggaggaaatgcctcctcgagcgggaacagccaggtga

**Drosophila Gene Hit** TBLASTN with ORF2: brahma protein (M85049) and imitation-SWI protein (ISWI) (L27127) and chromodomain-helicase-DNA-binding (CHD-1)

45 **Human Homologue** BLASTX with EST TBLASTN with ORF2: Snf2-related CBP activator protein (SRCAP) (AF143946) and SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4) (NM\_003072.1)

***Drosophila* EST** several including SD07794 (AI534784), LD34465 (AA990657)

**Annotated *Drosophila* genome genomic segment** AE003453

5 **Annotated *Drosophila* genome Complete gene candidate** CG9696 – domino an enzyme involved in DNA repair  
homology to snf2 family  
helicases

10 **Human homologue of Complete gene candidate** CG9696- gi4557447  
416409C913D6A935  
|ref|NP\_001261.1|  
chromodomain helicase DNA  
binding protein 1 [Homo  
sapiens] (1.90E-85

15 **Putative function** snf2 helicase family member protein that contains a  
chromodomain, which occurs in  
proteins that are implicated in chromatin compaction, and an  
20 SNF2/SWI2-like helicase domain, which occurs in proteins  
that are believed to activate transcription by counteracting  
the repressive effects of chromatin structure

**Confirmation by RNAi** Loss of G1, peak, increase in G2M indicating arrest in G2/M  
25

**Example 70 (Category 5)**

**Line ID** 99/31  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** NR  
**Map Position** 53E

**Rescue ID** EcoR1

**Rescue Sequence 1**

10 AAGGCCCCGACCAGAAACGAAATTTTCGGCGCGTNTTTTAAAATGCGCGGTAA  
ATTCACTTTGGATTTTGTGTTTTCTCTCTCGTTCTTCACACACACAGTTAGTTAGA  
TTGTGTGTTTCGCCTGGCTTTGCCTTTTAATTTTTTATTTACCTGCATCCGATTCTG  
GTATTTGAAACAGCCGTTGAGTCTCCTTTGGCTTTTTTATCAGCGACGTCATCA  
GTGGCGGCAGAAGCAGAAGCGTCGACAGCGGCGGGGGATTCCGGCTGCATCTT  
15 TGGAGCCCCTTTCCGGCTGTGCCCCACGGCTTTCGCCACCCCCGCAGTAACC  
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20 ATGCAATTTGTGTATCTGTCTCCTCCCCGANCGAACACGATNGAAAAAGGAA  
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NTTTATACCNCAACGAACGNGGAAAAAACNATATCNGNAATTACCCCCCGAA  
AATTGTTGCCNCTTTTACCCAAATATTTACAACCNCCGTTTCATTCCTCCTGGA  
25 ACATTCCNGGCCTTCCCAATTTTCNCCTTTACTACAATTTCAATGGTTTCTTTTT  
CCTCAC

**Rescue ID** BamH1

**Rescue Sequence 2**

30 CCTNAAATGTNGCGCTGGGNCCTAAANCGTCNCTCCTTGTGTCTCTCTTGTTTA  
CCGCGCTATGCTGATGTTGGCATGTGGTTCGATCCCCCTCCGTGTCGATGTTTA  
CAAAACCATNATTAGAGTTTGATGATTGAGTTCTCTTAACTTTCCTTCCTCCTT  
CCTTCCTTGGCTTTTGTTCATGCTAAATCCTTTAAATGGGGTTCTGCGTAGTTT  
AATGCCGAGGTACAGCAAACTTCAATATTCATGTTCCCTTGCGCTCCCAAAC  
35 GAAATTAGCATTGGACGTCCCAAGGTTGAAGACATTTNATTATTTTAACATCT  
TTTTNATTTTATTACATTTGAACTCTTACAAGTAATAATAATTACAATTAATAT  
TATAGCTGCAGCGGACAAAAAGGAGAAATCCCCCTCGCCGGTAATAAAGAAT  
CCAACAATAAGGATGCTNAAAANGAAGAAAACCCNAAAAAGGAGAAGAAAA  
ATCGGAANAAGGNGATGAGCCNGAAGATGAGGNNGATGAGAAAGCTAGCGA  
40 TGAAGAGAGCGAGAAGAAGAAANCGANATGAGATGCAGAGGACAGATAAAG  
GATGCCACNGATGAATCCAAGCCAAAATCGGGAGCCGATAAGCCCAAGAAAC  
TGAGCCCAAGGCCAAGAATGGCAAGGTGGNT

**Genomic hit, Accession No.** CSC:AC020063

**Associated ORF**

Genscan ORF1 predicted sequences >16:48:25|GENSCAN\_predicted\_peptide\_1|722\_aa  
 MPSPEKDANKAAETAAKENAADKVSVDENASVTAGVAKAVGAQPERGSKDA  
 AESPAAVDASASAATDDVADKKAKGDSTAVSNTESDAAAADKKEKSPSPVIKKS  
 NNKDAKKEDNSEKDEENSEDGDEPEDEADEKASDEESEKKKPKLDAEDKIKDAT  
 5 DESKPKSGADKPKKPEPKAKNGKVAKEEDDDEEDEDDEDAEDDDGDENDGLDK  
 NNEVAEDDENVVLAIEIDRINENINKTRVDGLQTLHAICFGAQGKNNVVKKNLRS  
 FAGFEFAKDSAEYNNKKLEAIKKVDNKGRLSICEILTDRKGSKNETVLRVLKFLM  
 EPDESLCLEQGDEEEEDAEDEDLDEDEEDPPSEEDKKRKSGKSSGGAGRGSARN  
 STGRPRRATAGKKMSAYVDFSSSDSEQKVA VPKRRRNDDSESGSDYNPSANS  
 10 SDGGRGGGAGAGRKVPSRGGRRPARKSRRRNSDSEEEEESEVSDADSDVPKR  
 KRGSVGRGRPAAPASAGRRGRGRGAASRK RKDSSEDEEVSEDEEEEDVSDFA  
 SDQSEVCKFNLISSIWCFIKYMPIFQEERPKSKKPITPAKNSKANNSKPKAGKADS  
 RSKKSKKESSEEDDDVDDKDESEDEDEPLTKKGKQAFPTDEQIRGYVKEILDKANL  
 EEITMKTVCKQVYAKYPDFDLTDKKDFIKATVKADGVQDLDGSPELIPRGRTTVT  
 15 IWLICCCNNQIFGET

>16:48:25|GENSCAN\_predicted\_CDS\_1|2169\_bp  
 atgccatcgccgcacgaaaaggatgctaacaaggcgcagaaacggcagccaaagaaaatgccgccgataaggtaagcgatg  
 tggaaaatgcatcggttactgctgggggtggcgaaagccgtgggggcacagccgaaaggggctccaaagatgcagccgaatc  
 20 ccccgccgctgtcgacgcctctgcctctgccgacctgatgacgtcgtgataaaaaagccaaaggagactcaacggctgttca  
 aataccgaatcgatgcagctgcagcggacaaaaaggagaatccccctcgccgtaataaagaagtccaacaataaggatgc  
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 25 agaggacgaggatgatgaggatgccgaagatgacgatggagacgagaacgatggcctggacaagaacaacgaggtggccg  
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 attcagcggagtacaacaaaaagctggaggccatcaaaaagggtggataataaggccctgcgcagcatctgcgagatccttacc  
 tcgatcgcaagggcagcaagaacgagactgtccttcgagtctcaaatcctaatggaaccggacgagtcgcttgcgttgagca  
 30 ggggtgatgaggaggaggaggaagatgccgaggacgaggatctggatgaagatgaggaggacccgccagtgaagaggaca  
 agaagcgcaagagcggaaagtctagcggcggcgctggcagaggctctgcacgcaattccaccggacgtccaaggcgcgga  
 cggcaggaaagaaaatgtccgcctatgtagatttccagctctgacgatagcgagcagaaagttgcagttccaaaaggagacg  
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 35 gaggaatcggaagtttccgatgccgatagtgtccaaaacgtaacgtgttccgtgggtaaacgtggacgaccggcagct  
 cctgcgtcagctggacgaaggggtagaggacgaggtgcagcttccgcaagcgtaaagattcagatagcgaagatgaggagg  
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 gtgttttatcaagtatatgccaattttcaggagggaacgtccaaaaagagcaagaagccattacgctgcgaaaaatagcaaa  
 ctaacaacaagtcaaaaccagctggaaaggccgatagtcgatcgaaaaaatcaagaagggaatcgtccgaggaagatgatgat  
 40 gtcgatgacaaagatgaatccgacgagatgagccactaaccaaaaggcgaacaggcattcccaacggatgaacaaatagc  
 cgatatgtcaagagattctgataaagccaatcttgaggagattacgatgaaaccgtgtgcaacaagtttatgcaaaatcc  
 agactttgacctaacagacaagaagacttcatcaaggcgacagtgaagcggacggagttcaggatttgatggtatgccga  
 actgatcccgctggccgaacaacgggtacaatatggttgatctgctgttgcaacaatcagatatttggggagacgtaa

45 **Human Homologue** TBLASTN with ORF1: poor homology with DEK gene  
 (D6S231E) (NM\_003472.1)  
**Drosophila EST** several including LD33301 (AA979048)

	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003805
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG5935 - EG:EG0003.6 - novel with weak homology to DEK oncogene
5		CG8648 - EG:EG0003.3 - novel XPG/ flap endonuclease-like, DNA repair?
10	<b>Human homologue of Complete gene candidate</b>	CG5935- 1e-17 4503249 ref NP_003463.1 pD6S231E  DEK gene >gi 544150 sp P35659 DEK_H UMAN DEK PROTEIN >gi 284375
15		CG8648- 4758356  ref NP_004102.1 pFEN1  flap structure-specific endonuclease 1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN(aa)
25	<b>Putative function</b>	CG5935: function unknown but putative DNA-binding protein predicted to be involved in chromosomal organisation. The translocation (6;9), associated with a specific subtype of acute myeloid leukemia, results in the fusion of two genes, dek and can, and the expression of a chimeric, leukemia-specific dek-can mRNA
30		CG8648: Novel XPG/ flap endonuclease-like, DNA repair protein
	<b>Confirmation by RNAi</b>	Both show slight reduction of G1 peak

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Each of the applications and patents mentioned above, and each document cited or referenced in each of the foregoing applications and patents, including during the prosecution of each of the foregoing applications and patents (“application cited documents”) and any manufacturer’s instructions or catalogues for any products cited or mentioned in each of the foregoing applications and patents and in any of the application cited documents, are hereby incorporated herein by reference. Furthermore, all documents cited in this text, and all documents cited or referenced in documents cited in this text, and any manufacturer’s instructions or catalogues for any products cited or mentioned in this text, are hereby incorporated herein by reference.

Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

**CLAIMS**

1. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 70 or the complement thereof.

5 (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 70, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 70 or a fragment thereof.

10 (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

2. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 14 or the complement thereof.

15 (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 14, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 14 or a fragment thereof.

20 (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

3. A polynucleotide selected from:

- (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 15 to 19 or the complement thereof.
- (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 15 to 19, or a fragment thereof.
- 5 (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 15 to 19 or a fragment thereof.
- (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
- 10 4. A polynucleotide selected from:
  - (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 20 to 30 or the complement thereof.
  - (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 20 to 30, or a fragment thereof.
  - 15 (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 20 to 30 or a fragment thereof.
  - (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
- 20 5. A polynucleotide selected from:
  - (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 31 to 53 or the complement thereof.
  - (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 31 to 53, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 31 to 53 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

6. A polynucleotide selected from:

(a) polynucleotides comprising any one of the nucleotide sequences set out in 54 to 70 or the complement thereof.

(b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in 54 to 70, or a fragment thereof.

(c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 54 to 70 or a fragment thereof.

(d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

7. A polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide according to any of Claims 1 to 6.

8. A polypeptide which comprises any one of the amino acid sequences set out in Examples 1 to 70 or in any of Examples 1 to 14, Examples 15 to 19, Examples 20 to 30, Examples 31 to 53 and Examples 54 to 70, or a homologue, variant, derivative or fragment thereof.

9. A polynucleotide encoding a polypeptide according to Claim 8.

10. A vector comprising a polynucleotide according to any of Claims 1 to 7 and 9.

11. An expression vector comprising a polynucleotide according to any of Claims 1 to 7 and 9 operably linked to a regulatory sequence capable of directing expression of said polynucleotide in a host cell.
12. An antibody capable of binding a polypeptide according to Claim 8.
- 5 13. A method for detecting the presence or absence of a polynucleotide according to any of Claims 1 to 7 and 9 in a biological sample which comprises:
- (a) bringing the biological sample containing DNA or RNA into contact with a probe according to Claim 9 under hybridising conditions; and
  - (b) detecting any duplex formed between the probe and nucleic acid in the  
10 sample.
14. A method for detecting a polypeptide according to Claim 8 present in a biological sample which comprises:
- (a) providing an antibody according to Claim 12;
  - (b) incubating a biological sample with said antibody under conditions which  
15 allow for the formation of an antibody-antigen complex; and
  - (c) determining whether antibody-antigen complex comprising said antibody is formed.
15. A polynucleotide according to according to any of Claims 1 to 7 and 9 for use in therapy.
- 20 16. A polypeptide according to Claim 8 for use in therapy.
17. An antibody according to Claim 12 for use in therapy.

18. A method of treating a tumour or a patient suffering from a proliferative disease comprising administering to a patient in need of treatment an effective amount of a polynucleotide according to any of Claims 1 to 7 and 9.

19. A method of treating a tumour or a patient suffering from a proliferative disease,  
5 comprising administering to a patient in need of treatment an effective amount of a polypeptide according to Claim 8.

20. A method of treating a tumour or a patient suffering from a proliferative disease, comprising administering to a patient in need of treatment an effective amount of an antibody according to Claim 12 to a patient.

10 21. Use of a polypeptide according to Claim 8 in a method of identifying a substance capable of affecting the function of the corresponding gene.

22. Use of a polypeptide according to Claim 8 in an assay for identifying a substance capable of inhibiting the cell division cycle.

15 23. Use as claimed in Claim 22, in which the substance is capable of inhibiting mitosis and/or meiosis.

24. A method for identifying a substance capable of binding to a polypeptide according to Claim 8, which method comprises incubating the polypeptide with a candidate substance under suitable conditions and determining whether the substance binds to the polypeptide.

20 25. A method for identifying a substance capable of modulating the function of a polypeptide according to Claim 8 or a polypeptide encoded by a polynucleotide according to any of Claims 1 to 7 and 9, the method comprising the steps of: incubating the polypeptide with a candidate substance and determining whether activity of the polypeptide is thereby modulated.

26. A substance identified by a method or assay according to any of Claims 21 to 25.
27. Use of a substance according to Claim 26 in a method of inhibiting the function of a polypeptide.
28. Use of a substance according to Claim 26 in a method of regulating a cell division  
5 cycle function.